

1
Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2004, 23:44:40 ; Search time 538.767 Seconds
(without alignments)
756.808 Million cell updates/sec

Title: US-09-940-235-2_COPY_16_383

Perfect score: 1901

Sequence: 1 SQLVSVAGTVEGTNQDISL.....IITVMGKRPEGENASYHLA 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
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- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
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- 30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
- 31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
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- 35: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*
- 36: /cgn2_6/ptodata/1/paa/US160_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Match	Length	DB	ID	Description
1	1901	100.0	413	29	US-10-360-101-264	Sequence 264, App
2	1901	100.0	413	29	US-10-360-101A-264	Sequence 264, App
3	1901	100.0	414	1	PCT-US93-09502-1	Sequence 1, Appli
4	1901	100.0	414	3	US-07-956-692A-9	Sequence 9, Appli
5	1901	100.0	414	5	US-08-128-299-1	Sequence 1, Appli
6	1901	100.0	414	18	US-09-471-349-2	Sequence 2, Appli
7	1901	100.0	414	24	US-09-940-235-2	Sequence 2, Appli
8	1901	100.0	414	32	US-10-631-558-2	Sequence 2, Appli
9	1901	100.0	440	22	US-09-791-537-45187	Sequence 45187, A
10	1875	98.6	401	20	US-09-658-681-1	Sequence 1, Appli
11	1875	98.6	413	20	US-09-658-681-2	Sequence 2, Appli
12	1875	98.6	414	18	US-09-438-136-252	Sequence 252, App
13	1875	98.6	414	20	US-09-633-516B-7	Sequence 7, Appli
14	1875	98.6	414	22	US-09-791-537-418	Sequence 418, App
15	1875	98.6	414	29	US-10-300-215-252	Sequence 252, App
16	1875	98.6	415	22	US-09-791-537-32688	Sequence 32688, A
17	1868.5	98.3	415	17	US-09-305-958-4	Sequence 4, Appli
18	1868.5	98.3	415	17	US-09-305-970-5	Sequence 5, Appli
19	1864	98.1	414	18	US-09-438-136-253	Sequence 253, App
20	1864	98.1	414	20	US-09-633-516B-8	Sequence 8, Appli
21	1864	98.1	414	29	US-10-300-215-253	Sequence 253, App
22	1859	97.8	440	22	US-09-791-537-45192	Sequence 45192, A
23	1845	97.1	413	9	US-08-567-943-12	Sequence 12, Appl
24	1845	97.1	413	24	US-09-919-703-12	Sequence 12, Appl
25	1822	95.8	362	22	US-09-791-537-43287	Sequence 23287, A
26	1819	95.7	384	20	US-09-658-681-4	Sequence 4, Appli
27	1815	95.5	372	20	US-09-658-681-3	Sequence 3, Appli
28	1741	91.6	440	30	US-10-415-182A-8298	Sequence 8298, Ap
29	1741	91.6	440	30	US-10-474-792-658	Sequence 658, App
30	1726	90.8	440	22	US-09-791-537-45189	Sequence 45189, A
31	1597	84.0	440	22	US-09-791-537-33832	Sequence 33832, A
32	1590	83.6	414	22	US-09-791-537-33829	Sequence 33829, A
33	1576	82.9	440	22	US-09-791-537-64009	Sequence 64009, A
34	708	37.2	138	22	US-09-791-537-104248	Sequence 104248,
35	695	36.6	137	22	US-09-791-537-12562	Sequence 12562, A
36	620	32.6	128	22	US-09-791-537-83460	Sequence 83460, A
37	569	29.9	128	22	US-09-791-537-83461	Sequence 83461, A
38	557	29.3	128	22	US-09-791-537-83463	Sequence 83463, A
39	552	29.0	128	22	US-09-791-537-83462	Sequence 83462, A
40	429.5	22.6	400	22	US-09-791-537-49654	Sequence 49654, A
41	423	22.3	128	22	US-09-791-537-83480	Sequence 83480, A
42	419	22.0	128	22	US-09-791-537-83467	Sequence 83467, A
43	419	22.0	128	22	US-09-791-537-83482	Sequence 83482, A
44	417	21.9	128	22	US-09-791-537-83466	Sequence 83466, A
45	408	21.5	128	22	US-09-791-537-83483	Sequence 83483, A

ALIGNMENTS

RESULT 1
US-10-360-101-264
; Sequence 264, Application US/10360101
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 264
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of streptokinase

US-10-360-101-264

Query Match 100.0%; Score 1901; DB 29; Length 413;
Best Local Similarity 100.0%; Pred. No. 5e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFFEDLTSPAHGKTEQGLSPKSPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDLTSPAHGKTEQGLSPKSPFATDSGAMSHKLE 75

Qy 61 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVFADKDGSVTLPTQVQEF 120
Db 76 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVFADKDGSVTLPTQVQEF 135

Qy 121 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDPPGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDPPGLKDTKLLKTLAIGDTIT 195

Qy 181 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 240
Db 196 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 255

Qy 241 KKSGLNEINNTDLISEKYYVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSQLLT 300
Db 256 KKSGLNEINNTDLISEKYYVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSQLLT 315

Qy 301 ASERNLDFRDLYDRDKAKLLYNNLDAGFIMDYTLTGKVEDNHDNTRIIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDRDKAKLLYNNLDAGFIMDYTLTGKVEDNHDNTRIIITVYMGKRPEG 375

Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 2

US-10-360-101A-264
; Sequence 264, Application US/10360101A
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101A
; CURRENT FILING DATE: 2003-02-07
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 264
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of streptokinase

US-10-360-101A-264

Query Match 100.0%; Score 1901; DB 29; Length 413;
Best Local Similarity 100.0%; Pred. No. 5e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFFEDLTSPAHGKTEQGLSPKSPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDLTSPAHGKTEQGLSPKSPFATDSGAMSHKLE 75

Qy 61 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVFADKDGSVTLPTQVQEF 120
Db 76 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVFADKDGSVTLPTQVQEF 135

Qy 121 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDPPGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDPPGLKDTKLLKTLAIGDTIT 195

Qy 181 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 240
Db 196 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 255

Qy 241 KKSGLNEINNTDLISEKYYVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSQLLT 300
Db 256 KKSGLNEINNTDLISEKYYVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSQLLT 315

Qy 301 ASERNLDFRDLYDRDKAKLLYNNLDAGFIMDYTLTGKVEDNHDNTRIIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDRDKAKLLYNNLDAGFIMDYTLTGKVEDNHDNTRIIITVYMGKRPEG 375

Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 3

PCT-US93-09502-1
; Sequence 1, Application PC/TUS9309502
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the
; TITLE OF INVENTION: DNA Encoding Such Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09502
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: 0609.3570001
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2545
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; STRANDEDNESS: both
; TOPOLOGY: both

PCT-US93-09502-1

Query Match 100.0%; Score 1901; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFFEDLTSPAHGKTEQGLSPKSPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDLTSPAHGKTEQGLSPKSPFATDSGAMSHKLE 75

Qy 61 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVFADKDGSVTLPTQVQEF 120
Db 76 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVFADKDGSVTLPTQVQEF 135

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Db 136 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDPPGLKDTKLLKTLAIGDTIT 195

Qy 181 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 240

Db 196 SOELLAQAQSILNKNHPGTYIYERDSSIVTHNDIFRITILPMDQEFYRVKREQAYRIN 255
Qy 241 KKSGLNEEINNTDLISEKYVYLKKEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVYLKKEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRDLVDPDRKAKLLYNNLDAGFIMDYTLTGKVEDNHDNTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLVDPDRKAKLLYNNLDAGFIMDYTLTGKVEDNHDNTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 4

US-07-956-692A-9
; Sequence 9, Application US/07956692A
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; APPLICANT: Kussie, Paul
; APPLICANT: Farhami-Seren, Behnaz
; TITLE OF INVENTION: Recombinant Streptokinase Fragments with
; TITLE OF INVENTION: Decreased Antigenicity and Uses Thereof
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1225 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956.692A
; FILING DATE: 19921005
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3570000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 833-7533
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: both
; TOPOLOGY: both
; US-07-956-692A-9

Query Match 100.0%; Score 1901; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDISLKFFEDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 75
Qy 61 KADLLKALQEQLIANVHNSDDYFEVIDFASDATITDRNGKVFADKOGSVTLPTQVQEF 120
Db 76 KADLLKALQEQLIANVHNSDDYFEVIDFASDATITDRNGKVFADKOGSVTLPTQVQEF 135
Qy 121 LLSGHRVRPYKKEPIQNOAKSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHRVRPYKKEPIQNOAKSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAIGDTIT 195

Qy 181 SOELLAQAQSILNKNHPGTYIYERDSSIVTHNDIFRITILPMDQEFYRVKREQAYRIN 240
Db 196 SOELLAQAQSILNKNHPGTYIYERDSSIVTHNDIFRITILPMDQEFYRVKREQAYRIN 255
Qy 241 KKSGLNEEINNTDLISEKYVYLKKEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVYLKKEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRDLVDPDRKAKLLYNNLDAGFIMDYTLTGKVEDNHDNTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLVDPDRKAKLLYNNLDAGFIMDYTLTGKVEDNHDNTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 5

US-08-128-299-1
; Sequence 1, Application US/08128299
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the
; TITLE OF INVENTION: DNA Encoding Such Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/128,299
; FILING DATE: Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: 0609.3570001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2545
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-128-299-1

Query Match 100.0%; Score 1901; DB 5; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDISLKFFEDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 75
Qy 61 KADLLKALQEQLIANVHNSDDYFEVIDFASDATITDRNGKVFADKOGSVTLPTQVQEF 120
Db 76 KADLLKALQEQLIANVHNSDDYFEVIDFASDATITDRNGKVFADKOGSVTLPTQVQEF 135
Qy 121 LLSGHRVRPYKKEPIQNOAKSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHRVRPYKKEPIQNOAKSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAIGDTIT 195
Qy 181 SOELLAQAQSILNKNHPGTYIYERDSSIVTHNDIFRITILPMDQEFYRVKREQAYRIN 240

Db 196 SQELLAQAQSILNKNHPCGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 255
Qy 241 KKSGLNEEINNTDLISEKYVVKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVVKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRDLYPDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYPDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 6
US-09-471-349-2
; Sequence 2, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sabni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-471-349-2

Query Match 100.0%; Score 1901; DB 18; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDISLKFIDLTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFIDLTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 75
Qy 61 KADLLKAIQEOQLIANVHSNDYFEVIDPASDATITDRNGKYVFADKDGSVTLPTQVQEF 120
Db 76 KADLLKAIQEOQLIANVHSNDYFEVIDPASDATITDRNGKYVFADKDGSVTLPTQVQEF 135
Qy 121 LLSGHVRVRPKPKPIQNAQKSDVEYTVQFTPLNPDDDFRGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPKPKPIQNAQKSDVEYTVQFTPLNPDDDFRGLKDTKLLKTLAIGDTIT 195
Qy 181 SQELLAQAQSILNKNHPCGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 240
Db 196 SQELLAQAQSILNKNHPCGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 255
Qy 241 KKSGLNEEINNTDLISEKYVVKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVVKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRDLYPDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYPDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

Db 376 ENASYHLA 383
RESULT 7
US-09-940-235-2
; Sequence 2, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sabni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940/235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-940-235-2

Query Match 100.0%; Score 1901; DB 24; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDISLKFIDLTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFIDLTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 75
Qy 61 KADLLKAIQEOQLIANVHSNDYFEVIDPASDATITDRNGKYVFADKDGSVTLPTQVQEF 120
Db 76 KADLLKAIQEOQLIANVHSNDYFEVIDPASDATITDRNGKYVFADKDGSVTLPTQVQEF 135
Qy 121 LLSGHVRVRPKPKPIQNAQKSDVEYTVQFTPLNPDDDFRGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPKPKPIQNAQKSDVEYTVQFTPLNPDDDFRGLKDTKLLKTLAIGDTIT 195
Qy 181 SQELLAQAQSILNKNHPCGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 240
Db 196 SQELLAQAQSILNKNHPCGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 255
Qy 241 KKSGLNEEINNTDLISEKYVVKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVVKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRDLYPDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYPDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383
RESULT 8
US-10-631-558-2
; Sequence 2, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sabni, Girish
; APPLICANT: Roy, Chait

```
; APPLICANT: Rajagopal, Kammarla
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-10-631-558-2

Query Match      100.0%; Score 1901; DB 32; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 75

Qy 61 KADLLKAIQEQLIANVHSNDYFEVIDFASDATITDRNGKVFADKDGSVTLPTQPVQEF 120
Db 76 KADLLKAIQEQLIANVHSNDYFEVIDFASDATITDRNGKVFADKDGSVTLPTQPVQEF 135

Qy 121 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 195

Qy 181 SQELLAQAQSILNKNHGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKNREQAYRIN 240
Db 196 SQELLAQAQSILNKNHGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKNREQAYRIN 255

Qy 241 KKSGLNEEINNTDLISEKYVYLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVYLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315

Qy 301 ASERNLDFRDLYDRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDHDTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDHDTNRIITVYMGKRPEG 375

Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 9
US-09-791-537-45187
; Sequence 45187, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45187

; APPLICANT: Rajagopal, Kammarla
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-10-631-558-2

Query Match      100.0%; Score 1901; DB 32; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 75

Qy 61 KADLLKAIQEQLIANVHSNDYFEVIDFASDATITDRNGKVFADKDGSVTLPTQPVQEF 120
Db 76 KADLLKAIQEQLIANVHSNDYFEVIDFASDATITDRNGKVFADKDGSVTLPTQPVQEF 135

Qy 121 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 195

Qy 181 SQELLAQAQSILNKNHGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKNREQAYRIN 240
Db 196 SQELLAQAQSILNKNHGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKNREQAYRIN 255

Qy 241 KKSGLNEEINNTDLISEKYVYLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVYLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315

Qy 301 ASERNLDFRDLYDRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDHDTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDHDTNRIITVYMGKRPEG 375

Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 9
US-09-791-537-45187
; Sequence 45187, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45187
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; LENGTH: 440
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-09-791-537-45187

Query Match      100.0%; Score 1901; DB 22; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.6e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 42 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 101

Qy 61 KADLLKAIQEQLIANVHSNDYFEVIDFASDATITDRNGKVFADKDGSVTLPTQPVQEF 120
Db 102 KADLLKAIQEQLIANVHSNDYFEVIDFASDATITDRNGKVFADKDGSVTLPTQPVQEF 161

Qy 121 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 180
Db 162 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 221

Qy 181 SQELLAQAQSILNKNHGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKNREQAYRIN 240
Db 222 SQELLAQAQSILNKNHGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKNREQAYRIN 281

Qy 241 KKSGLNEEINNTDLISEKYVYLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 282 KKSGLNEEINNTDLISEKYVYLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 341

Qy 301 ASERNLDFRDLYDRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDHDTNRIITVYMGKRPEG 360
Db 342 ASERNLDFRDLYDRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDHDTNRIITVYMGKRPEG 401

Qy 361 ENASYHLA 368
Db 402 ENASYHLA 409

RESULT 10
US-09-658-681-1
; Sequence 1, Application US/09658681
; GENERAL INFORMATION:
; APPLICANT: Madrazo, Isis Del Carmen Torrens
; APPLICANT: Garcia, Jose De Jesus De La Fuente
; APPLICANT: Ojalvo, Ariana Garcia
; APPLICANT: Menendez, Alina Seraleña
; APPLICANT: Escalona, Elder Pupo
; APPLICANT: Masso, Julio Raul Fernandez
; APPLICANT: Griego, Martha De Jesus Gonzalez
; TITLE OF INVENTION: STREPTOKINASE MUTANTS
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5
; CURRENT APPLICATION NUMBER: US/09/658,681
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-09-658-681-1

Query Match      98.6%; Score 1875; DB 20; Length 401;
Best Local Similarity 98.6%; Pred. No. 1.4e-167;
Matches 363; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 3 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 62

Qy 61 KADLLKAIQEQLIANVHSNDYFEVIDFASDATITDRNGKVFADKDGSVTLPTQPVQEF 120
Db 63 KADLLKAIQEQLIANVHSNDYFEVIDFASDATITDRNGKVFADKDGSVTLPTQPVQEF 122
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Qy 121 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAGDIT 180
Db 123 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAGDIT 182
Qy 181 SOELLAQAQSLNKNHPCYTIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 240
Db 183 SOELLAQAQSLNKNHPCYTIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 242
Qy 241 KKSGLNEEINNLTDLISEKYVYLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 243 KKSGLNEEINNLTDLISEKYVYLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 302
Qy 301 ASERNLDFRDLYDRDRKAKLLYNLDAPGIMDYTLTGKVEDNHDNTNRIIVYMGKRPEG 360
Db 303 ASERNLDFRDLYDRDRKAKLLYNLDAPGIMDYTLTGKVEDNHDNTNRIIVYMGKRPEG 362
Qy 361 ENASYHLA 368
Db 363 ENASYHLA 370
RESULT 11
US-09-658-681-2
; Sequence 2, Application US/09658681
; GENERAL INFORMATION:
; APPLICANT: Madrazo, Isis Del Carmen Torrens
; APPLICANT: Garcia, Jose De Jesus De La Fuente
; APPLICANT: Ojalvo, Ariana Garcia
; APPLICANT: Menendez, Alina Seraleña
; APPLICANT: Escalona, Elder Pupo
; APPLICANT: Masso, Julio Raul Fernandez
; APPLICANT: Griego, Martha De Jesus Gonzalez
; TITLE OF INVENTION: STREPTOKINASE MUTANTS
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5
; CURRENT APPLICATION NUMBER: US/09/658.681
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-681-2
Query Match 98.6%; Score 1875; DB 20; Length 413;
Best Local Similarity 98.6%; Pred. No. 1.4e-167;
Matches 363; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDLSLKFFELDLTSRPAHGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 3 SOLVSVAGTVEGTNQDLSLKFFELDLTSRPAHGKTEQGLSPKSPKPFATDSGAMPHKLE 62
Qy 61 KADLLKAIQEQLIANVHNSDDYFEVIDFASDATITDRNGKVYFADKQGSVLTPTQVQEF 120
Db 63 KADLLKAIQEQLIANVHNSDDYFEVIDFASDATITDRNGKVYFADKQGSVLTPTQVQEF 122
Qy 121 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAGDIT 180
Db 123 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAGDIT 182
Qy 181 SOELLAQAQSLNKNHPCYTIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 240
Db 183 SOELLAQAQSLNKNHPCYTIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 242
Qy 241 KKSGLNEEINNLTDLISEKYVYLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 243 KKSGLNEEINNLTDLISEKYVYLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 302
Qy 301 ASERNLDFRDLYDRDRKAKLLYNLDAPGIMDYTLTGKVEDNHDNTNRIIVYMGKRPEG 360
Db 303 ASERNLDFRDLYDRDRKAKLLYNLDAPGIMDYTLTGKVEDNHDNTNRIIVYMGKRPEG 362
Qy 361 ENASYHLA 368

Db 363 ENASYHLA 370
RESULT 12
US-09-438-136-252
; Sequence 252, Application US/09438136
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; ADAIR, Fiona Suzanne
; HAMILTON, Anita Anne
; CARTER, Graham
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
; NON-IMMUNOGENIC PROTEINS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr L.L.P.
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,136
; FILING DATE: 10-NOV-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB98/01473
; FILING DATE: 21-MAY-1998
; APPLICATION NUMBER: GB 9710480.6
; FILING DATE: 21-MAY-1997
; APPLICATION NUMBER: GB 9716197.0
; FILING DATE: 31-JUL-1997
; APPLICATION NUMBER: GB 9725270.4
; FILING DATE: 28-NOV-1997
; APPLICATION NUMBER: GB 9807751.4
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/067,235
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102286.395CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-09-438-136-252
Query Match 98.6%; Score 1875; DB 18; Length 414;
Best Local Similarity 98.6%; Pred. No. 1.5e-167;
Matches 363; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDLSLKFFELDLTSRPAHGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDLSLKFFELDLTSRPAHGKTEQGLSPKSPKPFATDSGAMPHKLE 75
Qy 61 KADLLKAIQEQLIANVHNSDDYFEVIDFASDATITDRNGKVYFADKQGSVLTPTQVQEF 120
Db 76 KADLLKAIQEQLIANVHNSDDYFEVIDFASDATITDRNGKVYFADKQGSVLTPTQVQEF 135
Qy 121 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAGDIT 180
Db 136 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDFFRGLKDTKLLKTLAGDIT 195


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; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: GB 9710480.6
; PRIOR FILING DATE: 1997-05-21
; PRIOR APPLICATION NUMBER: GB 9716197.0
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: GB 9725270.4
; PRIOR FILING DATE: 1997-11-28
; PRIOR APPLICATION NUMBER: GB 9807751.4
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/067,235
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-10-300-215-252

Query Match          98.6%; Score 1875; DB 29; Length 414;
Best Local Similarity 98.6%; Pred. No. 1.5e-167;
Matches 363; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFFEDILTSRPAHGGKTEQGLSPKSPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDILTSRPAHGGKTEQGLSPKSPFATDSGAMPHKLE 75
Qy 61 KADLLKAIQQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 120
Db 76 KADLLKAIQQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 135
Qy 121 LLSGHVVRPYKEKPIQNAQKSVDEVYTVQFTPLNPDDEPGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVVRPYKEKPIQNAQKSVDEVYTVQFTPLNPDDEPGLKDTKLLKTLAIGDTIT 195
Qy 181 SQELLAQAQSILNKNHPGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKRNREQAYRIN 240
Db 196 SQELLAQAQSILNKNHPGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKRNREQAYEIN 255
Qy 241 KKSGLNEEINNTDLISEKYVYLKKGKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVYLKKGKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRLYDRDKAKLLYNLDAGFIMDYTLTGKVEDNHDHTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRLYDRDKAKLLYNLDAGFIMDYTLTGKVEDNHDHTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383
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Search completed: November 4, 2004, 00:11:20
Job time : 540.767 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:21:37 ; Search time 6024.11 Seconds
(without alignments)
2477.164 Million cell updates/sec

Title: US-09-940-235-2_COPY_16_383

Perfect score: 1901

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 44308572 seqs, 20275418765 residues

Total number of hits satisfying chosen parameters: 88617144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Pending Patents NA Main -QMT=fastap -SUFFIX=p2n.rnpsm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7

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Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 406 TTGCTAGCGGACATGCGGGTTAGACCATATAAAGAAACCAATACAAACCAACGCG 465
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 466 AAATCTGTTGATGGAAATACCTGACAGTTTACTCCCTTAAACCTGTAGCGATTTC 525
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 526 AGACCAGGCTCTCAAGAGTACTAAGCTATTGAAACACTAGTATCGGTGACACCATCA 585
Qy 181 SerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 586 TCTCAAGAAATACCTGCTCAAGCAAAAGCAATTTTAAACAAACCAACCCAGGCTATACG 645
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 646 ATTTATGACGCTGACTCTCTCAATCGTCACTCATGCAATGACATTTTCGTAACGATT 705
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 706 -CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAAACCAAGCTTATAGGATCA 765
Qy 241 LysLysSerGlyLeuAsnGluLeuAsnGluLeuAsnThrAspLeuIleSerGluLysTyr 260
Db 766 AAAAAATCTGCTCGAATGAAGAATAAACCAACTGACCTGATCTCTGAGAAATATTAC 825
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 826 GTCTTAAAAAGGGAAGGAAACCGGTATGATCCCTTTGATCGCAGTCACTTGAACTGTT 885
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 886 ACCATCAATACGTTGATGTCGATACCAACGAAATGCTTAAAGGTGAGCAGCTCTTAACA 945
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 946 GCTAGCAACGTAACCTTAGACTTCAGAGATTATACGATCTCGTGATGAAGGCTAAACTA 1005
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1006 CTCACAAACAATCTCGATGCTTTGGTATTATGACTATACCTTAACCTGGAAGTAGAG 1065
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1066 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATATGGCAACGACCGAAGGA 1125
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1126 GAGAATGCTAGCTATCATTTAGCC 1149

RESULT 2

US-09-940-235-1

; Sequence 1, Application US/09940235

; GENERAL INFORMATION:

; APPLICANT: Kumar, Rajesh

; APPLICANT: Sabni, Girish

; APPLICANT: Roy, Chait

; APPLICANT: Rajagopal, Kammar

; APPLICANT: Nihalani, Deepak

; APPLICANT: Sundaram, Vasudha

; APPLICANT: Yadav, Mahavir

; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE

; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID

; TITLE OF INVENTION: PROTEIN

; FILE REFERENCE: 07064-009002

; CURRENT APPLICATION NUMBER: US/09/940,235

; CURRENT FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 09/471,349

; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1242)
US-09-940-235-1

Alignment Scores:

Pred. No.:	5,79e-186	Length:	1245
Score:	1901.00	Matches:	368
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	40	Gaps:	0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-940-235-1 (1-1245)

Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 46 AGCCAAATAGTTGTTAGCGTTGCTGCTACTGTTGAGGGGACGAATCAAGACATTAGCTCT 105
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 106 AAATTTTGAATCGATCAACATCAGCACCTGCTCATGAGGAAAGACAGACGAAGGC 165
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 166 TTAAGTCCAAATCAAAACCAATTTGCTACTGATAGTGGCGCATGTGCATATAAATTGAG 225
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 226 AAAGCTGACTTACTTAAGGCTATTCAAGAACAAATGATCGCTTACGTCACAGTAACGAC 285
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 286 GACTACTTTGAGGTCAATGATTTTGCAGGCGATGCAACCATCTACTGATCGAAACGCAAG 345
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 346 GTCTACTTTGCTGCAAAAGATGGTTTCGGTAACCTTTCGCCGACCAACCTGTCCAAAGATT 405
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 406 TTGCTAAGCGGACATGTCGGCTTAGACCATATAAAGAAACCAATACAAACCAACGCG 465
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 466 AAATCTGTTGATGGAAATACCTGATACAGTTTACTCCCTTAAACCTGTATGACGATTTC 525
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 526 AGACCAGGCTCTCAAGAGTACTAAGCTATTGAAACCACTAGCTATCGGTGACACCATCA 585
Qy 181 SerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 586 TCTCAAGAAATTACTAGCTCAAGCAAAAGCAATTTTAAACAAACCAACCCAGGCTATACG 645
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 646 ATTTATGACGCTGACTCTCTCAATCGTCACTCATGACATGACATTTTCGTAACGATT 705
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 706 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAAACCAAGCTTATAGGATCA 765
Qy 241 LysLysSerGlyLeuAsnGluLeuAsnThrAspLeuIleSerGluLysTyrTyr 260


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Db 766 AAAAAATCTGGTCTGAATGAAGAAATAAACCAACTGACCTGATCTCTGAGAAATATTAC 825
Qy 261 ValLeuLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 826 GTCTTAAAAAAGGGGAAAGCCGATGATCCCTTTGATCCAGTCACCTTGAAACTGTTC 885
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 886 ACCATCAATACGTTGATGTCATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACA 945
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 946 GCTAGCGAACGTAACCTTAGACTTCAGAGATTATATACGATCTCTGCGTAAGGCTAAACTA 1005
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValClu 340
Db 1006 CTCTACAAACAATCTCGATGCTTTGGTATTATGACTATATACCTTAACTGGGAAAAAGTAGAG 1065
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1066 GATPAATCAGGATGACCAACCGTATCATACCGTTTATATGGCGAAGCCGACCGAAGGA 1125
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RESULT 3

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US-10-631-558-1
; Sequence 1, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sabni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN/3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1242)
US-10-631-558-1
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Alignment Scores:
Pred. No.: 5,79e-186 Length: 1245
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0
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US-09-940-235-2_COPY_16_383 (1-368) x US-10-631-558-1 (1-1245)

Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20

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Db 46 AGCCAAATAGTGTGTAGCGTTGCTGGTACTGTGTAGGGGACGAATCAAGACATTAGTCTT 105
Qy 21 LysPheGheGluIleAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 106 AATTTTTTGAATTCGATCAACATCAGCACTGCTCATGAGGAGAAAGACAGACGACG 165
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 166 TTAAGTCCAAATCAAAACCAATTTGCTACTGATAGTGGCGGATGTCACATAAATTGAG 225
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 226 AAAGCTGACTTACTAAAGGCTATTCAAGACAAATTTGATCGCTAAACGTCACAGTAACGAC 285
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 286 GACTACTTTGAGGTCAATGATTTTGCAGGCGATGCAACATTTACTGATCGAAACCGCAAG 345
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 346 GTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGATTT 405
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
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Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 466 AAATCTGTTGATGGGAATATACTGTACAGTTTACTCCCTTAACCCCTGATGACCATTT 525
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 526 AGACCAAGTCTCAAGATACTTAAGCTATTGAAACACTAGCTATCGGTGACACCATCACA 585
Qy 181 SerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 586 TCTCAAGAATTACTAGCTCAAGCAAAAGCATTTTAAACAAACCAACCCAGGCTATACG 645
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 646 ATTTATGAACGTGACTCTCTCAATCGTCACTCATGACATGACATTTTCGTACGATTTTA 705
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 706 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAAACAAGCTTATAGGATCAAT 765
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 766 AAAAAATCTGGTCTGAATGAAGAAATAAACCACTGACCTGATCTCTGAGAAATATTAC 825
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLysLeuPhe 280
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Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 886 ACCATCAATACGTTGATGTCATACCAACGAATTGCTTAAAAAGTGAGCAGCTCTTAACA 945
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 946 GCTAGCGAACGTAACCTTAGACTTCAGAGATTATATACGATCTCTGTAAGGCTAAACTA 1005
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1006 CTCTACAAACAATCTCGATGCTTTGGTATTATGACTATATACCTTAACTGGAAAGTAGAG 1065
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1066 GATPAATCAGGATGACCAACCGTATCATACCGTTTATATGGCGAAGCCGACCGAAGGA 1125
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
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Db 1126 GAGATGCTAGCTATCATTTAGCC 1149

RESULT 4

US-09-569-920-2
; Sequence 2, Application US/09569920
; GENERAL INFORMATION:
; APPLICANT: Reddy, Vemuri B.
; APPLICANT: Lerner, Echan
; TITLE OF INVENTION: VASODILATOR-THROMBOLYTIC FUSION PROTEIN
; TITLE OF INVENTION: AND CONJUGATES
; FILE REFERENCE: 10284-026001
; CURRENT APPLICATION NUMBER: US/09/569,920
; CURRENT FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-09-569-920-2

Alignment Scores:
Pred. No.: 5.85e-186 Length: 1254
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-569-920-2 (1-1254)

Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspSerLeu 20
Db 52 AGCCAAATTAGTTGTTAGGTTGCTGCTACTGTTGGGGGAGCAATCAAGACATTAGTCTT 111
Qy 21 LysPheGluLeuAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 112 AAAATTTTGAATCGATCTAACATCAGCCTGCTCATGGAGGAAAGACAGAGCAAGGC 171
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 172 TTAAGTCAAAATCAAAACCACTTTGCTACTGATAGTGGCGGATGTCTCAATAAACTTGA 231
Qy 61 LysAlaAspLeuLeuLysAlaGlnGluGlnLeuLeuAlaAsnValHisSerAsnAsp 80
Db 232 AAAGTGACTTACTAAAGGCTATTCAAGAACAAATGCTGCTAACGTCACAGTAACGAC 291
Qy 81 AspTyrPheGluValLysLeuAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 292 GACTACTTTGAGTCAATTTGTTTGAAGCGATGCAACCATTAATGTCGAAACGGCAAG 351
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 352 GTCTACTTTGCTGCAAAAGATGTTGCTGTAACCTTGGCGACCAACCTGTCTCAAGAATT 411
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 412 TTGCTAAGCGGACATGTCGCGGTAGACCATATAAGAAACCAACCAATCAAAACCAAGCG 471
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 472 AAATCTGTTGATGGGAATATCTGTACAGTTTACTCCCTTAACCCCTGATGACGATTC 531
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 532 AGACAGGCTCTCAAGATACTAAGCTATTGAAACACACTAGCTATCGGTGACACCATACA 591
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 592 TCTCAAGAAATTACTAGCTCAAGCAAGCAAGCAATTTTAAACAAAAACCAACCCAGGCTATACG 651
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220

Db 652 ATTTATGAACGTGACTCTCTCAATCTCACTCATGACAATGACATTTTCGTACGATTTTA 711
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 712 CCAATGGATCAAGAGTTTACTTACCGTGTAAATAATCGGAACAAGCTTATAGGATCAAT 771
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuLysSerGluLysTyrTyr 260
Db 772 AAAAATCTGGTCTCAATCAAGAAATAAACACACACTGACCTGATCTCTGAGAAATATTAC 831
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspAspSerHisLeuLysLeuPhe 280
Db 832 GTCTCTTAAAAAAGGGGAAAGCCGATGATCCCTTTGATCGCAGTCACCTTGAACCTGTT 891
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 892 ACCATCAATAGCTTGATGTCGATACCAACGAATGCTTAAAGATGAGCAGCTCTTAACA 951
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 952 GCTAGCGAAACGTAACTTAGACTTCAGAGATTTATACGATCTCTGATAGGCTAAACTA 1011
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1012 CTCTACAAACAATCTCGATGCTTTTGGTATTATGGACTATACCTTAACCTGAAAAAGTAGAG 1071
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1072 GATAATACGATGACCAACCGTATCATACCGTTTATATGGCAAGCGACCCGAAGGA 1131
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1132 GAGATGCTAGCTATCATTTAGCC 1155

RESULT 5

US-09-471-349-6
; Sequence 6, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-471-349-6

Alignment Scores:
Pred. No.: 6.28e-186 Length: 1327
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-471-349-6 (1-1327)

```
Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 128 AGCAATTTGGTTGTACGGTTGCTGTACTGTTGAGGGGACGATCAAGACATTAGTCTT 187
Qy 21 LysPhePheGluLeuLeuAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 188 AAATTTTGAATTCGATTAACATCAGCCTCTCATGAGGAGAAAGACAGCAAGGC 247
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 248 TTAAGTCCAAATCAAAACCATTTGCTACTGATAGTGGCGGATGTCACATAAACTTGAG 307
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 308 AAAGCTGACTTACTAAAGGCTATTCAAGACAAATTGATCGTAACTGCTCCACGTAACGAC 367
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 368 GACTACTTTGAGGTCATTGATTTTGCAAGCGATGCAACCACTTACTGATCGAAACGGCAAG 427
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 428 GTCTACTTTGCTGCAAAAGATGGTTCGGTAACCTTGGCGACCCCAACCTGTCACAGAATTT 487
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 488 TTGCTAAGCGGACATGTGCGGTTAGACCATATTAAGAAACCAACCAATACAAACCAAGCG 547
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 548 AAATCTGTGATGGAATATACTGTACAGTTTACTCCCTTAAACCCCTGATGACGATTC 607
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 608 AGACCAAGTCTCAAGATATCTAAGCTATTGAAACACTAGTATCGGTGACACCATCACA 667
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 668 TCTCAAGAAATTACTAGTCTCAAGCAAAAGCAATTTTAAACAAACCCACCGGTATACG 727
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 728 ATTTATGAACGTGACTCTCAATCGTCACTCATGACAAATGACATTTTCGGTACGATTTTA 787
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 788 CCAATGGATCAAGAGTTTACTTACCGGTGTTAAAAATCGGAAACAAAGCTTATAGGATCAAT 847
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 848 AAAAATCTGCTCGAATGAAGAAATAAACACACTGACCTGATCTCTGAGAAATATTAC 907
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 908 GTCCTTAAAAAGGGGAAAGCCGTATGATCCCTTTGATCGCACTCACTTGAAACTGTC 967
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 968 ACCATCAATACGTTGATGTCGATACCAACGAATGCTAAAAAGTGACGCTCTTAACA 1027
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1028 GCTAGCGGAACGTAACTTAGACTTCAGAGATTATACCATCTCTGTGTAAGGCTTAAACTA 1087
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1088 CTCTACAACAATCTCGATGCTTTTGGTATTATGACTATACCTTAACTGGAAGATAGAG 1147
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1148 GATAATCACGATGACACCAACCGTATCATACCGTTTATATATGGGCAAGCGACCGCAAGGA 1207
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
```

```
Db 1208 GAGAAATGCTAGCTATCATTTAGCC 1231
RESULT 6
US-09-940-235-6
; Sequence 6, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sabni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
US-09-940-235-6
Alignment Scores:
Pred. No.: 6,28e-186 Length: 1327
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: 40 Gaps: 0
US-09-940-235-2_COPY_16_383 (1-368) x US-09-940-235-6 (1-1327)
Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 128 AGCAATTTGGTTGTACGGTTGCTGTACTGTTGAGGGGACGATCAAGACATTAGTCTT 187
Qy 21 LysPhePheGluLeuLeuAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 188 AAATTTTGAATTCGATTAACATCAGCCTCTCATGAGGAGAAAGACAGCAAGGC 247
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 248 TTAAGTCCAAATCAAAACCATTTGCTACTGATAGTGGCGGATGTCACATAAACTTGAG 307
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 308 AAAGCTGACTTACTAAAGGCTATTCAAGACAAATTGATCGTAACTGCTCCACGTAACGAC 367
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 368 GACTACTTTGAGGTCATTGATTTTGCAAGCGATGCAACCACTTACTGATCGAAACGGCAAG 427
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 428 GTCTACTTTGCTGCAAAAGATGGTTCGGTAACCTTGGCGACCCCAACCTGTCACAGAATTT 487
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 488 TTGCTAAGCGGACATGTGCGGTTAGACCATATTAAGAAACCAACCAATACAAACCAAGCG 547
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
```

```
Db 548 AATCTGTTGATGGGAATATACCTGACAGTTTACTCCCTTAAACCCCTGATGACGATTC 607
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 608 AGACCAGCTCTCAAGATACCTAAGCTATTGAAACACTAGCTATCGGTGACACCATCACA 667
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 668 TCTCAAGAAATTTACTAGCTCAAGCACAAGCAATTTTAAACAAAACCCAGCTATACG 727
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 728 ATTTATGAACGTGACTCTCAATCGTCTACTCATGCAATGACATTTTCCGACGATTTTA 787
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 788 CCAATGATCAAGAGTTTACTTACCGTGTATAAATCGGAACAAGCTTATAGGATCAAT 847
Qy 241 LysLysSerGlyLeuAsnGluLuleAsnThrAspLeuIleSerGluLysTyrThr 260
Db 848 AAAAAATCTGCTGAATGAAGAAATAAACACACTGACCTGATCTCTGAGAAATATTAC 907
Qy 261 ValLeuLysLysGlyGluLysProTyrAspPropheAspArgSerHisLeuLysLeuPhe 280
Db 908 GTCCCTTAAAAAGGGGAAAGCCGATGATGCCCTTTGATCGCAGTCACTTGAACCTGTT 967
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 968 ACCATCAATACGTTGATGTCGATACCAACGAATTTGCTAAAGTGAGCAGCTCTTAACA 1027
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1028 GCTAGGACGTAAGCTTACAGATCTTACGATTTATACGATCTCTGATAGCTTAACCTA 1087
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1088 CTCTACACAATCTCGATGCTTTTGGTATTATGACTATACCTTAACCTGGAAAGTAGAG 1147
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1148 GATAATCAGATGACACCAACCGTATCATACCGTTTATATGGGCAAGCGACCGAAGGA 1207
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1208 GAGAACTGCTAGCTATCATTTAGCC 1231
```

RESULT 7

```
US-10-631-558-6
; Sequence 6, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahn, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
```

; LENGTH: 1327

; TYPE: DNA

; ORGANISM: Streptococcus equisimilis

US-10-631-558-6

Alignment Scores:

Pred. No.:	6,286-186	Length:	1327
Score:	1901.00	Matches:	368
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	57	Gaps:	0

US-09-940-235-2_COPY_16_383 (1-368) x US-10-631-558-6 (1-1327)

```
Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 128 AGCCAAATGGTGTGTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTT 187
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 188 AAAATTTTGAATCGATCTAATCATCAGCCTGCTCATGGAGGAAGACAGAGCAGGC 247
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 248 TTAAGTCCAAATCAAAACCAATTTGCTACTGATAGTGGCGCGATGTCACATAAATTGAG 307
Qy 61 LysAlaAspLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 308 AAAGCTGACTTACTAAAGCTATTCAAGAACAAATTTGATCGCTAAACGCTCCACAGTAACGAC 367
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 368 GACTACTTTGAGTCAATGATTTTGCACGCGATGCAACCAATTTACTGATCGAAACGCGAAG 427
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 428 GTCTACTTTGCTGACAAAGATGTTTCGGTAACTTTGCCGACCAACCTCTCCAGAAATTT 487
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 488 TTGCTAAAGCGACATGTCGCGCTTAGACCATATAAGAAAAAACCAATACAAAAACCAAGCG 547
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 548 AAATCTGTTGATGTGGAATATATCTGACAGTTTACTCCCTTAAACCCCTGATACGATTC 607
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 608 AGACCAGCTCTCAAGATACCTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACA 667
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 668 TCTCAAGAAATTTACTAGCTCAAGCACAAGCAATTTTAAACAAAACCCAGCTATACG 727
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 728 ATTTATGAACGTGACTCTCAATCGTCTACTCATGCAATGACATTTTCCGTCAGATTTTA 787
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 788 CCAATGATCAAGAGTTTACTTACCGTGTATAAATCGGAACAAGCTTATAGGATCAAT 847
Qy 241 LysLysSerGlyLeuAsnGluLuleAsnThrAspLeuIleSerGluLysTyrThr 260
Db 848 AAAAAATCTGCTGAATGAAGAAATAAACACACTGACCTGATCTCTGAGAAATATTAC 907
Qy 261 ValLeuLysLysGlyGluLysProTyrAspPropheAspArgSerHisLeuLysLeuPhe 280
Db 908 GTCCCTTAAAAAGGGGAAAGCCGATGATGCCCTTTGATCGCAGTCACTTGAACCTGTT 967
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
```

Db 968 ACCATCAATACGTTGATGTCGATACCAACGAATTGCTAAAGGTGAGCAGCTCTTAACA 1027
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1028 GCTAGCGAACGTAACCTTAGACTTCAGAGATTATACGATCTCTGATGAAGCGCTAAACTA 1087
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1088 CTCTACAACAATCTCGATGCTTTTGGTATTATGACATATACCTTAACCTGGAAGAGTAGAG 1147
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1148 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATGGCGAAGCGACCGAAGGA 1207
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1208 GAGAATGCTAGCTATCATTTAGCC 1231

RESULT 8

US-09-471-349-5
; Sequence 5, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahn, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
US-09-471-349-5

Alignment Scores:
Pred. No.: 6.57e-186 Length: 1377
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-471-349-5 (1-1377)

Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 178 AGCCAAATGGTGTAGCTTGGTACTCTTGGGGGACGAATCAAGACATTAGTCTT 237
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyLysThrGluGlnGly 40
Db 238 AAATTTTGGATTCGATCTACATCAGCAGCTCTCATGGAGGAGNAGACAGCAAGGC 297
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 298 TTAAGTCCAAATCAAAACCACTTTGCTACTGATAGTGGCGGATGTCACATAAACTTCAG 357
Qy 61 LysAlaAspLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 358 AAAGCTGACTTACTAAAGGCTATTCAAGAACAAATTGATCGTAAACGCTCCACAGTAACGAC 417
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100

Db 418 GACTACTTTGAGTCAATGATTTTCAAGCGATGCAACCATTTATGATGCAAAACGCGAAG 477
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 478 GTCTACTTTGCTGACAAAGATGGTTGGTAACCTTGGCGACCAACCTGTCTCCAGNATTT 537
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGlyLysProIleGlnAsnGlnAla 140
Db 538 TTGCTAAGCGCATGTCGCGGTTAGACCATATAAAGAAACCAACCAATACAAACCAAGCG 597
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 598 AAATCTGTGTGATGGAATATCTGTACAGTTTACTCCCTTAAACCCCTGATGACGATTTTC 657
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 658 AGCCAGGTCTCAAGATACCTAAGCTATTGAAACACATAGCTATCGTGACACCATCACA 717
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 718 TCTCAAGAAATTTACTAGCTCAAGCACAAGCATTTTAAACAAACCAACCCAGGCTATACG 777
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 778 ATTTATGAACGTGACTCTCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTA 837
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 838 CCAATGGATCAAGAGTTTACTTACCGTGTAAATAACGGAAACAAAGCTTATAGGATCAAT 897
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGlyLysTyrTyr 260
Db 898 AAAAAATCTGCTCAATGAAGAAATAAACCAACTGACCTGATCTCTGAGAAATATTAC 957
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 958 GTCTTAAAAAAGGGGAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAACCTGTTTC 1017
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 1018 ACCATCAAAATACGTTGATGTCGATACCAACGAATTTGTAAGAGTGAGCAGCTCTTTAACA 1077
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1078 GCTAGCGAACGTAACCTTAGACTTCAGAGATTATACGATCTCTCGTATGAAGCTAAACTA 1137
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1138 CTCTACAACAATCTCGATGCTTTGGTATTATGGAATATACCTTAACCTGGAAGAGTAGAG 1197
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1198 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATGGCAAGCGACCGAAGGA 1257
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1258 GAGAATGCTAGCTATCATTTAGCC 1281

RESULT 9

US-09-940-235-5
; Sequence 5, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahn, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN


```
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 238 AAATTTTTCGAATCGATTAACATCAGACCTGCTCATGGAGGAAAGACAGACGAGGC 297

Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 298 TTAAGTCAAAATCAAAACCACTTTCGTACTGATAGTGGCGGATGTCCACATAAACTTCAG 357

Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 358 AAAGCTGACTTACTAAAGGCTATTCAAGACAAATGATCGTAAACGTCACAGTAACGAC 417

Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 418 GACTACTTTGAGGTCATTTGATTTTGAAGCGATCAACCACTTACTGATCGAAACGGCAAG 477

Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 478 GTCTACTTTGCTGACAAAGATGGTTCGTAACTTCGCGACCCCAACCTGTCCAAAGATTT 537

Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 538 TTGCTAAGCGGACATGCGCGTTAGACCATATATAAGAAACCAATACAAACCAAGCG 597

Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 598 AAATCTGTTGATGGATATATCTGTACAGTTTACTCCCTTAAACCCCTGATGAGATTC 657

Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 658 AGACCAAGTCTCAAGATATACTAAGCTATTGAAACACATAGCTATCGGTGACACCATACA 717

Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 718 TCTCAAGAATTACTAGCTCAAGCAAAAGCATTTTAAACAAAAACCAACCCAGGCTATACG 777

Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 778 ATTTATGAAGCTGACTCTCTCAATCGTCACTCATGACCAATGACATTTTCGTACAGATTTTA 837

Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 838 CCAATGGATCAAGAGTTTACTTACCGTGTAAATAATCGGAAACAAGCTTATAGGATCAAT 897

Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 898 AAAAAATCTCGTCTGAAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTAC 957

Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLysLeuPhe 280
Db 958 GTCTTAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGAGTCACTTGAACACTGTTC 1017

Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 1018 ACCATCAAAATACGTTGATGTCGATACCAACGAATGCTAAAAAGTGAGCAGCTCTTAACA 1077

Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1078 GCTAGCGAAGCTAACTTAGACTTTCAGAGATTATATACGATCTCTGATGAAGGCTAAACTA 1137

Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1138 CTCTACAACTCTCGATGCTTTTGGTATTATGAGCTATACCTTAACTGGAAGAAGTAGAG 1197

Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1198 GATAATCACCATGACACCAACCGTATCATAAACCGTTTATATGCGCAGACGCCGGAAGA 1257

Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1258 GAGAACTGCTAGCTATCATTTTATGACC 1281
```

```
RESULT 11
US-09-471-349-9
; Sequence 9, Application US/094711349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-471-349-9
```

```
Alignment Scores:
Pred. No.: 7,57e-186 Length: 1541
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
```

US-09-940-235-2_copy_16_383 (1-368) x US-09-471-349-9 (1-1541)

```
Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 78 AGCCAAATGGTGTGTAGCGTTGCTGGTACTGTGTAGGGGACGAAATCAAGACATTAAGTCTT 137

Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 138 AAATTTTTCGAATCGATTAACATCAGACCTGCTCATGGAGGAAAGACAGACGAGGC 197

Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 198 TTAAGTCCAAATCAAAACCACTTTCGTACTGATAGTGGCGCATGTCAATAAATTTGAG 257

Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 258 AAAGCTGACTTACTAAAGGCTATTCAAGAAACAATTTGATCGCTAAACGTCACAGTAACGAC 317

Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 318 GACTACTTTGAGGTCATTTGATTTTGAAGCGATGCAACCATGCAATTTACTGATCGAAACGGCAAG 377

Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 378 GTCTACTTTGCTGACAAAGATGGTTCGTGAACCTTTGCCGACCAACCTGTCTCAAGAAATTT 437

Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 438 TTGCTAAGCGGACATGTCGCGGTTAGACCATATATAAGAAACCAATACAAACCAAGCG 497

Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 498 AAATCTGTTGATGGAAATATATCTGACAGTTTACTCCCTTAAACCCCTGATGACGATTC 557

Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
```



```
Db 558 AGACGAGTCTCAAGAGATACTAAGCTATTGAAACACACTAGCTATCGGTGACACCATCACA 617
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 618 TCTCAAGAAATTACTAGCTCAAGCACAAGCAATTTAAACAAAACCCAGGCTATACG 677
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 678 ATTTATGAACGTGACTCTCAATCGTCACTCATGACAATGACATTTTCGCTACGATTTTA 737
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 738 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAACAAGCTTATAGGATCAAT 797
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 798 AAAAAATCTGCTCGAATGAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTAC 857
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLeuPhe 280
Db 858 GTCTCTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACCTTGAAACTGTTC 917
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 918 ACCATCAAAATACGTTGATGTCGATACCAACGAATTTGCTAAAAAGGTGACGCTCTTAACA 977
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 978 GCTAGCGNACGTAACCTTAGACTTCAGAGATTATACGATCTCTGATGAAAGGTGACGCTCTTAACA 1037
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1038 CTCTACACATCTCGATGCTTTTGGTATTATGATGACTATACCTTAACCTGGAAGATAGAG 1097
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1098 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATATGGGCAAGCGCCGGAAGGA 1157
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1158 GAGAACTGCTAGCTACCATTTAGCT 1181
RESULT 12
; Sequence 9, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-09-940-235-9
```

Alignment Scores:

Pred. No.: 7, 57e-186 Length: 1541
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-940-235-9 (1-1541)

```
Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 78 AGCCAAATGGTGTAGCGTTGCTGCTACTGTTGAGGGGACGAATCAAGACATTAGTCTT 137
Qy 21 LysPheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 138 AAAATTTTGAATCGATCAACATCAGCAGCTGCTCATGGAGGAAAGACAGACGAGGC 197
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyValaMetSerHisLysLeuGlu 60
Db 198 TTAAGTCCAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAATTGAG 257
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 258 AAAGCTGACTTACTAAAGGCTATTCAAGAACAAATTCGCTAAACGTCACACAGTAACGAC 317
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 318 GACTACTTTGAGGTCAATGATTTTGCACGCGATGCAACCATTTACTGATCGAAACGCGAAG 377
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 378 GTCTACTTTGCTGACAAAGATGGTTCGGTAACTTCCCGACCCCACTGTCGAGAAATTT 437
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 438 TTGCTAAGCGGACATGTGCGGGTTAGACCATATAAGAAACCAATAACAAACCAAGCG 497
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspAspPhe 160
Db 498 AAATCTGTTGATGTGGAATATATCTGTACAGTTTACTCCCTTAAACCCCTGATGACGATTTC 557
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 558 AGACGAGTCTCAAAAGATACTAAGCTATTGAAACACACTAGCTATCGTGACACCATCACA 617
Qy 181 SerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 618 TCTCAAGAAATTACTAGCTCAAGCACAAGCAATTTTAAACAAAACCCAGGCTATACG 677
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 678 ATTTATGAACGTGACTCTCAATCGTCACTCATGACAATGACATTTTCGCTACGATTTTA 737
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 738 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAACAAGCTTATAGGATCAAT 797
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 798 AAAAAATCTGCTCGAATGAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTAC 857
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 858 GTCTCTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACCTTGAAACGTGTC 917
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 918 ACCATCAAAATACGTTGATGTCGATACCAACGAATTTGCTAAAAAGGTGACGCTCTTAACA 977
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
```



```
Db 978 GCTAGCGAAGCTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTA 1037
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1038 CTCTACAAACAATCTCGATGCTTTTGGTATTATGACCTATACCTTAACCTGGAAGTAGAG 1097
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1098 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATGCGCAAGCGACGCAAGGA 1157
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1158 GAGAATGCTAGCTACCATTTAGCT 1181

RESULT 13
US-10-631-558-9
; Sequence 9, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-10-631-558-9

Alignment Scores:
Pred. No.: 7,57e-186 Length: 1541
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-10-631-558-9 (1-1541)
Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 78 AGCCAAATGGTTGTTAGCTGGTCTTCTGAGGGGACGAATCAAGACATTTAGTCTT 137
Qy 21 LysPheGluIleAspLeuThrSerArgProIleHisGlyLysThrGluGlnGly 40
Db 138 AAATTTTGGAAATCGATCTAACTACGACCTCTCATGGAGGAAAGACAGCAAGGC 197
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 198 TTAAGTCAAAATCAAAACCAATTTGCTACTGATAGTGGCGCGATGTCACTAACTTAG 257
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGlnGluGlnGluGlnGluGlnGluGlnGlu 80
Db 258 AAAGCTGACTTACTAAAGGCTATTCAAGAAACAATTGATCGCTAAAGTCCACAGTAACGAC 317
```

```
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 318 GACTACTTTGAGGTCAATTTGTTTTCGAAGCGATGCAACCATTTACTGATCGAAACGGCAAG 377
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 378 GTCTACTTTGCTGCAAAAGATGGTTTCGGTAACCTTTGCGGACCAACCTGCTCCAGAATTTT 437
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 438 TTGCTAAGCGGACATGTCGCGTTAGACCATATAAAGAAACCAATACAAACCAAGCG 497
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 498 AAATCTGTTGATGTGAATATACTGTACAGTTTACTCCCTTAAACCTGATGACGATTTTC 557
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 558 AGACGAGGTCTCAAAAGATACTAAGCTATTGAAACACTAGCTATCGGTGACACCATCACA 617
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 618 TCTCAAGAATTACTAGCTCAAGCAACAAAGCATTTTAAACAAACCAACCCAGCGCTAAG 677
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 678 ATTTATGACGTGACTCTCTCAATCGTCACTCATGACCAATGACATTTTCCGTACGATTTTA 737
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 738 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGGAACAAGCTTTATAGGATCAAT 797
Qy 241 LysLysSerGlyLeuAsnGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 798 AAAAAATCTGCTGGAATGAAGAAATAAACCACTGACCTGATCTCTGAGAAATATTAC 857
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 858 GTCCTTAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGCAGTCACCTTGAACATGTTTC 917
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 918 ACCATCAATACGTTGATGTCGATACCAACGAATTTGCTAAAAAGTCAGCAGCTCTTAAACA 977
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 978 GCTAGCGAAGCTAACTTAGACTTCAGAGATTTATACGATCCTCGTGATAAGGCTAAACTA 1037
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1038 CTCTACAAACAATCTCGATGCTTTTGGTATTATGACTATACCTTAACCTGGAAGTAGAG 1097
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1098 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATGCGCAAGCGACGCAAGGA 1157
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1158 GAGAATGCTAGCTACCATTTAGCT 1181

RESULT 14
US-09-471-349-10
; Sequence 10, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
```

; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-471-349-10

Alignment Scores:
Pred. No.: 8.31e-186 Length: 1661
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-940-235-2_copy_16_383 (1-368) x US-09-471-349-10 (1-1661)

Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 228 AGCCAAATGGTGTGGTACTGCTGGTACTGCTGGGAGGACCAAGACATAGTCTT 287
Qy 21 LysPheGluIleAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 288 AAAATTTTGAATCGATCTAACTACGACTCTCTCATGGAGGAACAGACGAAGGC 347
Qy 41 LeuSerProTyrSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 348 TTAAGTCCAAATCAAAACCACTTTGCTACTGATAGTGGCGGATGTACATAAACTTGAG 407
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 408 AAAGCTGACTTACTAAAGGCTATTCAAGAACAAATGATCGTAAACGTCACAGTAACGAC 467
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 468 GACTACTTTGAGGTCATGATTTTGCAGCGCATGCAACCATCTGATCGAAACGGCAAG 527
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 528 GTCTACTTTGCTGACAAGATGGTTCGGTAACCTTGGCGACCAACCTGTCACAGAATTT 587
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 588 TTGCTAAGCGACATGTGCGCGTTAGACCATATAAGAGAAAACCAATACAAACCAAGCG 647
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 648 AAATCTGTGATGGAATATACGTATGATGATGATGATGATGATGATGATGATGATGAT 707
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 708 AGACCAGGTCTCAAGATACTAAGCTATTGAAACACACTAGCTATCGGTGACCATCA 767
Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 768 TCTCAAGAAATTACTAGCTCAAGCAAAAGCATTTTAAACAAAACCAACCCAGGCTATACG 827
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 828 ATTTATGAACGTGCTCTCAATCGTCACTCATGCAATGACATTTTCCCGTACGATTTTA 887
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240

Db 888 CCAATGGATCAAGAGTCTTACTACCGTGTATAAAATCGGAAACAAGCTTATAGGATCAAT 947
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 948 AAAAATCTGGTCTGAATGAAGAAATAACAACACTGACCTGATCTCTGAGAAATATTAC 1007
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 1008 GTCCTTAAAAAAGGGGAAAGCCGATGATGATCCCTTTGATCGCAGTCACCTTGAACGTTC 1067
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
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Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1128 GCTACGCAACGTAACCTTAGACTTCAGAGATTTATACGATCCCTCGTATAGGCTAAACATA 1187
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1188 CTCTACAACATCTCGATGCTTTTGGTATTATGGACTATACCTTAACCTGAAAAAGTAGAG 1247
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1248 GATAATCAGGATGACACCAACCGTATACACCGTTTATATGGCAAGCGACCCGAAGGA 1307
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1308 GAGAATGCTAGCTATCATTTAGCC 1331

RESULT 15

; Sequence 10, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-09-940-235-10

Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-2_copy_16_383 (1-368) x US-09-940-235-10 (1-1661)

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Qy	21	LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLeuThrGluGlnGly	40				
Db	288	AAATTTTTGAAATCGATCTAACATCAGCATCGCTCATGGAGGAAAGACAGCAGCAGGC	347				
Qy	41	LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu	60				
Db	348	TTAAGTCCAAATCAAAACCATTTGCTACTGATAGTGGCGGATGTCACATAAACTTGAG	407				
Qy	61	LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp	80				
Db	408	AAAGCTGACTTACTAAAGGCTATTCAAGAACAAATTGATCGCTAAACGTCACAGTAAACGAC	467				
Qy	81	AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys	100				
Db	468	GACTACTTTGAGGTCATTGATTTTGAAGCGCATGCAACCATTTACTGATCGAAACGGCAAG	527				
Qy	101	ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe	120				
Db	528	GTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGATTT	587				
Qy	121	LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla	140				
Db	588	TTGCTAAGCGGACATGTCGCGGTTAGACCATATAAAGAAACCAATAACAAACCAAGCG	647				
Qy	141	LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe	160				
Db	648	AAATCTGTGTGATGGAAATATACTGTACAGTTTACTCCCTTAAACCCCTGATGACGATTTT	707				
Qy	161	ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr	180				
Db	708	AGACCAGTCTCAAGATACTAAGCTATTGAAACACTAGCTATCGGTGACACCATCACA	767				
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Qy	201	IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu	220				
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Db	1008	GTCCCTTAAAAAGGGGAAAAACCGTATGATCCCTTTGATCGCAGTCACCTTGAAACTGTC	1067				
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Qy	321	LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu	340				
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Qy	341	AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly	360				
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Qy	361	GluAsnAlaSerTyrHisLeuAla	368				

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:38:12 ; Search time 114.055 Seconds
(without alignments)
747.335 Million cell updates/sec

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Perfect score: 1901

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 63957 seqs, 115811272 residues

Total number of hits satisfying chosen parameters: 1387914

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1432	75.3	1299	8	US-60-615-573-2546 Sequence 2546, Ap
2	1403	73.8	1323	8	US-60-615-573-2545 Sequence 2545, Ap
3	1369	72.0	1323	8	US-60-615-573-2544 Sequence 2544, Ap
4	125.5	6.6	1344	8	US-60-615-573-7001 Sequence 7001, Ap
5	124	6.5	1343	8	US-60-615-573-7002 Sequence 7002, Ap
6	109.5	5.8	1512	8	US-60-615-573-18391 Sequence 18391, A
7	107.5	5.7	6806	6	US-10-956-160-1475 Sequence 1475, Ap
8	105	5.5	105	5	US-10-163-587B-3 Sequence 3, Appli
9	104.5	5.5	1248	8	US-60-615-573-13062 Sequence 13062, A
10	102	5.4	2697	8	US-60-615-573-7856 Sequence 7856, Ap

11	101.5	5.3	266145	6	US-10-856-118-1	Sequence 1, Appli
12	100.5	5.3	945	8	US-60-615-573-12450	Sequence 12450, A
13	100	5.3	1584	6	US-10-956-157-943	Sequence 943, App
14	100	5.3	3845	6	US-10-163-587B-5	Sequence 5, Appli
15	99.5	5.2	1860	8	US-60-615-573-7919	Sequence 7919, Ap
16	98	5.2	1012	8	US-60-615-573-1845	Sequence 1845, Ap
17	97.5	5.1	2682	8	US-60-615-573-14432	Sequence 14432, A
18	96	5.0	2000	8	US-60-615-573-18494	Sequence 18494, A
19	96	5.0	3093	6	US-60-615-573-17425	Sequence 17425, A
20	95.5	5.0	2140	6	US-10-510-386-75	Sequence 75, Appli
21	95.5	5.0	2568	8	US-60-615-573-12512	Sequence 12512, A
22	95.5	5.0	7888	6	US-10-956-157-1031	Sequence 1031, Ap
23	94.5	5.0	2214	8	US-60-615-573-14190	Sequence 14190, A
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25	94	4.9	1284	8	US-60-615-573-17277	Sequence 17277, A
26	94	4.9	1860	8	US-60-615-573-18498	Sequence 18498, A
27	94	4.9	7145	6	US-10-956-160-667	Sequence 667, App
28	94	4.9	30612	8	US-60-620-788-64	Sequence 64, Appl
29	93.5	4.9	2028	8	US-60-615-573-14199	Sequence 14199, A
30	93	4.9	1836	8	US-60-615-573-12429	Sequence 12429, A
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33	92	4.8	1632	8	US-60-615-573-9954	Sequence 9954, Ap
34	92	4.8	2604	8	US-60-615-573-14424	Sequence 14424, A
35	91.5	4.8	726	6	US-10-663-094-32	Sequence 32, Appl
36	91	4.8	1227	8	US-60-615-573-7848	Sequence 7848, Ap
37	91	4.8	1731	8	US-60-615-573-819	Sequence 819, App
38	91	4.8	1998	8	US-60-615-573-18415	Sequence 18415, A
39	91	4.8	6319	6	US-10-956-157-708	Sequence 708, App
40	91	4.8	140680	6	US-10-746-294A-83	Sequence 83, Appl
41	90.5	4.8	700	6	US-10-956-157-1731	Sequence 1731, Ap
42	90.5	4.8	700	6	US-10-956-157-6966	Sequence 6966, Ap
43	90.5	4.8	741	6	US-10-734-049A-384	Sequence 384, App
44	90.5	4.8	1400	6	US-10-956-157-6178	Sequence 6178, Ap
45	90	4.7	2457	8	US-60-615-573-13084	Sequence 13084, A

ALIGNMENTS

RESULT 1
US-60-615-573-2546
; Sequence 2546, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2546
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (597)..(597)
; OTHER INFORMATION: n is a, c, g, or t
US-60-615-573-2546

Alignment Scores:			
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Score:	1432.00	Matches:	290
Percent Similarity:	82.61%	Conservative:	14
Best local Similarity:	78.88%	Mismatches:	56
Query Match:	75.33%	Indels:	8
DB:	8	Gaps:	1
US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-2546 (1-1299)			

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Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 184 AAAATTTTGTAAATTGACCTAACATCACGACCTGCTCAGGGAGGAGAAACAGACGACGAGC 243
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Db 244 TTAGCTCAAAATCAAAA-----ATGCCATATAAACTGAA 279
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Db 280 AAAGCTGACTATTAAAGGCTATTCAAGAACAAATTGATCGCTAACGTTTCACAGTAACGAC 339
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Db 340 GGCTACTTTGAGGTCAATTGATTTTGCAAGCGATGCAACCATCACTGATCGAAACGGCAAG 399
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 400 GTCTACTTTGCTGATCGAGATGATTGCGTAACCTTGCCGACCAACCTGTCACAGAAATTT 459
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 460 TTGCTAAGCGGCATGTGCGGCTTAGACCGTATCRMCCCTARARCCGTTTCACAACTCWGCT 519
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 520 GAAGCGCTTAAACGTCAACTATGAAGTAGCTTTGTCTCCGAAACACAGGARATTTAGACTTT 579
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 580 ACRCMTVTGTTAARARANCRTATACATTTGACCACACATGGCGAGTTGGTGACTCTCTTTCA 639
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 640 TCACAAGAGTTAGCAGCRATTTGCCAAATTTATCTATCAAAARARYATCCAGATTAATC 699
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 700 ATTACAAACGKAGCTCTCAATGCTCAATGCTCAACATGACAAKAGAYATTTCCGTACGATTTA 759
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Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 820 AAAAAATCTGTCAGRWGRAAAATRAACACACACACCTKATCTCTGAGAAATATTAY 879
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Db 880 RTCTTAAAAAAGGGARRAGCKYRTRATCCCTTTGATCGCAGTCACTTGAAACTGTTC 939
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Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
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Qy 361 GluAsnAlaSerTyrHisLeuAla 368
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Db 1180 GAGAATGCTAGCTATCATTTAGCT 1203
RESULT 2
US-60-615-573-2545
; Sequence 2545, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2545
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (621)..(621)
; OTHER INFORMATION: n is a, c, g, or t
US-60-615-573-2545
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Query Match: 73.80% Indels: 0
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Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
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Db 964 ACCATCAAWTAGTGTGATGTCRAVACCAASRMWTTGCTAAAGACGACCTCTTAACA 1023
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1024 GCTAGCGAACRTAACTTAGACTTCAGAGATTATACGATCTCTGTGATAAGCTTAACTA 1083
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1084 CTCTACAAACAATCTCGATGCTTTTGGTATTATGTCGTATATACCTTAAGCTGGAAGTGCAG 1143
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1144 GATAATCAGATGACACCAACCGGTATCATACCGTTTATATGGGCAAGCGACCCGAAGGW 1203
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1204 GAGATGCTAGTATCATTTAGCY 1227
```

RESULT 3

US-60-615-573-2544

; Sequence 2544, Application US/60615573

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; APPLICANT: Murphy, Ellen

; APPLICANT: Olmsted, Stephen

; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES

; FILE REFERENCE: 031896-084099 (AM 101724)

; CURRENT APPLICATION NUMBER: US/60/615,573

; NUMBER OF SEQ ID NOS: 18598

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2544

; LENGTH: 1323

; TYPE: DNA

; ORGANISM: Streptococcus pyogenes

US-60-615-573-2544

Alignment Scores:

Pred. No.:	2,57e-153	Length:	1323
Score:	1369.00	Matches:	278
Percent Similarity:	77.17%	Conservative:	6
Best Local Similarity:	75.54%	Mismatches:	84
Query Match:	72.01%	Indels:	0
DB:	8	Gaps:	0

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-2544 (1-1323)

```
Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 124 AGCCARTTAGTGTAGTATGGCGGTATCGTTGAGGATCCGATACCGATAAAAGTTTTATA 183
```

```
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 184 AATTTTTTTGAAATCGATCAACACACACACACACACACACACACACACACACACACAC 243
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 244 TTAAGTCCAAATCAAAACCAATTTCTACATATATRGCGCATGCGACATAAATTTGAA 303
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 304 AAAGCTGACTTATTAAAGCTATTCAAAACGCTGATCGCTAACCTYCACGTAATYAGAC 363
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 364 GGCTACTTTGAGTGTATTTGTTTCGAAGCGATGCAACCATTTACTTGAYCGMRACGRYMAS 423
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 424 RTMTACTTTGCTTTRYYAAGATGRTYTCGGTAACTTTGCCSACCACCTCTTCCAAATTT 483
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 484 TTGTFWAVVGRCATGTTCGCGTTAGACCATATAAGAAACCAACCACTCAAAATCAGCR 543
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 544 ARATCTGYGATRTERRATATCTGTACAGTTTACCTTTCCTTTCACCTGATGAYGATTTC 603
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 604 AVRCMGKKMTCAAAARRTACTTAARCTATTGAAAMAYTAGCTATCGGYRRCCACRTCA 663
Qy 181 SerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 664 TCYCAAGAATTTACTAGCTCAAGACACAAAGCATTTTAAWCRAAASCCAYTCARRYATACG 723
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 724 ATTATGACGTGATCTCTCAATCGTACTCATGACRAKGRYATTTTCGTACRAATTTTA 783
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 784 CCAAYRGATCAARAGTTTACTTACCTRTYAAARAYCGGGAACAAGCTTATVRRRHCRAY 843
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 844 HMWAAACWGRMTMKRWARARAYDAAMAACACACYGAYCTTCTCTCGAGAAATATTAC 903
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 904 RTCCCTTAAAMAARGGARDMKCCGATGATCCCTTTGATCGCAGTCACTTGAACATGTTTC 963
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 964 ACCATCAAWTAGTGTGATGTCRAVACCAASRMWTTTCTTAAAGAYGAGACGCTCTTAACA 1023
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1024 GCTAGCGAASGTAACCTTAGACTTCAGAGATTATACGATCCCTYGTGATAGGCTAAACTA 1083
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1084 CTCTACAAACAATCTYGTGCTTTTGTATYATGACTTACCTTAACTCGGAAMGTAGAG 1143
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1144 GATAATCAGATRASAMYAAVCGTFTYTHACMGTTTATATGGGYAAGCGCMCCYRAAGGR 1203
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1204 GMRAAKGSTAGCTATCATTTAGCY 1227
```


Db 142 ATTATTGTAATGTTACAGGTACTGATCAAAACCGGAAT---AGCATTTTACCGCATAT 198
Qy 23 PheGluIleAspLeuThrSerArgProAlaHisGlyGlyLeuThrGluGlnGlyLeuSer 42
Db 199 ATCGAAGTCAATGTA----- 213
Qy 43 ProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAla 62
Db 214 -----AAGATGGGACAAACTTTAAGTAAARAA 240
Qy 63 AspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnVal-----HisSerAsnAsp 80
Db 241 GAAATTCAGATTATATTCCTCGAAATTTAAACTCTAGTGTGGAGGAGAAAGTAAACAA 300
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAla-----ThrIleThrAsp 96
Db 301 GTTCAATACCAACATCGAGTTTAAGAAAGTCTTATCTGAACGCTCAATTAGATGAT 360
Qy 97 ArgAsnGlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnPro 116
Db 361 GGCAAGACAGAGAAATAGCAATTGATAACGACGCT---GTTACTGTACTAAAGACGGT 417
Qy 117 ValGlnGluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIle 136
Db 418 CCAACAAATTTTGGATTGACGTTCCAGTAACCTTGTACGGTAAATTTCAATAACTCCAAAG 477
Qy 137 GlnAsnGlnAlaLys-----SerValAspValGluTyrThrValGlnPheThrPro 153
Db 478 CTCCATAAGTAGAATGGGGTACACTATTTTCAGTTTACATTTATGTACAGTTCGTT--- 534
Qy 154 LeuAsnProAspAspAspPheArgProGlyLeuLysAspThrLysLeuLysLysThrLeu 173
Db 535 -----GATAAACTACAGGTAAACTTTAGAGGATTTTAAACTATTGATTTTCT 585
Qy 174 AlaIle-----GlyAspThrIleThrSerGlnGluLeuLeuAla 186
Db 586 GAAATTCAGACCTTGGAAATTCGACATACCGGTGATAGCATTACCGATAGGAAGTATAAAC 645
Qy 187 GlnAlaGlnSerIleLeuAsnLysAsn-----HisProGlyTyrThrIleTyrGlu 203
Db 646 TCAGCTTACAGTGCTTTTAAAGSAGTAAATTAATAAGCAAGGYTATCAATTTCCAATAC 705
Qy 204 ArgAspSerSerIleValThrHisAsnAsnAspIlePheArgThrIleLeuProMetAsp 223
Db 706 AGAATTAGTACAGATGTTCAACAAATCTTCAAGTCCACAAACCTTTCAACTACGAT 765
Qy 224 -----GlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 766 GTAAATGAAGAAATGATTAACTATCAAAATCGAAACCAATAGACCCACACTAAACCTATCT 825
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyr 260
Db 826 AATRAAGCC-----GAGACTGATATCTTTTCGAAAGATATAT 864
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 865 GTTCTAGATGGA-----GATAGTTTACACCGTACAGAA---TCAACWATT 909
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 910 TCGATTAAATGGTTGATGCCAAACCTGAAMAASCGCTATTTTAAACCACACATTAACGGT 969
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 970 -----TATASACATTGKCAACT-GTTTCCAAT 995
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLys----- 338
Db 996 GTCTATACAGACTCTTTGAAGAAATCTTATCCCAACTCAAAATCAGGAGAAARATAT 1055
Qy 339 ---ValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArg 357
Db 1056 TTTATTCAAAATATGAAAAAACAACAGCTGAACAAGAATATACTGTTTACCTTCAGAAACA 1115

Qy 358 ProGluGlyGlu 361
Db 1116 CCTTATTCTGAA 1127

RESULT 6

US-60-615-573-18391
; Sequence 18391, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18391
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-60-615-573-18391

Alignment Scores:
Pred. No.: 0.0027 Length: 1512
Score: 109.50 Matches: 74
Percent Similarity: 34.45% Conservative: 45
Best Local Similarity: 21.45% Mismatches: 123
Query Match: 5.76% Indels: 103
DB: 8 Gaps: 15

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-18391 (1-1512)

Qy 48 PheAlaThrAspSerGlyAlaMetSer---HisLysLeuGluLysAlaAspLeuLys 66
Db 487 TATTACACTCTCGAAGGTACTATAAGTTCCAAAAATTTTAAATCCAGAACTTGAAAT 546
Qy 67 AlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspTyrPhe----- 83
Db 547 TCACAAATCACAACTTATTATTATTAACACCGATTTCTCAACTTAAGTATTTAATAATGAT 606
Qy 84 ---GluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyr 102
Db 607 CAGGAATTACTAGCATTTGCAATTTGAAAAATTTGTAT-----AAAAATCGGATATTTTC 660
Qy 103 PheAlaAspLysAspGlySerVal-----ThrLeuProThrGlnPro 116
Db 661 CTGAGTGATAAAATATAAATACTCCACCAATATTTCAATAATACTAGTGAACATACCT 720
Qy 117 ValGlnGluPheLeuLeuSerGlyHisVal---ArgValArgProTyrLysGluLysPro 135
Db 721 GTTTTAGCTGTTTGCATAGTACTCATGTCWAGAATATTGACATATGATATGATCGGAC 780
Qy 136 IleGlnAsnGlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsn 155
Db 781 ATCAAAAATACTTTATAAACATGTT-----TTTAACAATCTTAAAT 819
Qy 156 ProAspAspAspPheArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIle 175
Db 820 AGATACTCT----- 828
Qy 176 GlyAspThrIleThrSerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn 195
Db 829 GGGATAATTGTCGACTAAACCAACAATTTGGATATATATCAGCTCGAATAAATAATGAA 888
Qy 196 HisProGlyTyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIle 215
Db 889 ATCCCTGTTCTACTATA----- 906
Qy 216 PheArgThrIleLeuProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGln 235


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Db 907 -----CCAGTAGGATATATTGATGAACATTTTACTAAATTTTAAAAAGAAAT----- 951
Qy 236 AlatyArgileAsnLysLysSerGlyLeuAsnGluGluLeuAsnThrAspLeuile 255
Db 952 -----AATCATAGTATAAATAATAATAAATAATTTAT 981
Qy 256 SerGluLysTyrTyrValLeuLysLysGly-----GluLys 267
Db 982 TCCGTCGACGTTATCTCCGGAAGAACAGTTGAATCATCAAAATGAATTAGTTTCTAAA 1041
Qy 268 ProTyrAspPropheAspArgSerHisLeuLysLeuPheThrIle----- 282
Db 1042 TTAATTAAGAAATTTCTCCTGAAAGAACAGTTGAATCATCAAAATGAATTAGTTTCTAAA 1101
Qy 283 LysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSer 302
Db 1102 AAATCAAGCACTAAATCACTGAATATAATTTAGAAACAAATGTTTTCAGAGGGTTT 1161
Qy 303 GluArgAsnLeu-----AspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1162 AGAAGAAATTTAAGTCTGAGATTCAGATGCTTAT-----ATGTCCTA 1206
Qy 321 LeuTyrAsnAsnLeuAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1207 ATTACTAGTATATCGAAGGATTTAAATTTA-----GGTTTATTAGAA 1248
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1249 -----ACTATAACTGAAGGCATACCTCCAGTTGGC 1278
Qy 361 GluAsnAlaSerTyr 365
Db 1279 TATTAATTCGAAGTAT 1293

RESULT 7
US-10-956-160-1475
; Sequence 1475, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1475
; LENGTH: 6806
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-1475

Alignment Scores:
Pred. No.: 0.0426 Length: 6806
Score: 107.50 Matches: 63
Percent Similarity: 31.52% Conservative: 59
Best Local Similarity: 16.28% Mismatches: 118
Query Match: 5.65% Indels: 147
DB: 6 Gaps: 14

US-09-940-235-2_COPY_16_383 (1-368) x US-10-956-160-1475 (1-6806)

Qy 33 HisGlyGlyLysThr-----GluGlnGlyLeuSerProLysSer 45
Db 904 CATCTGTCGATCATCATGATGATAGACCTCCCGGCACAGCCGGTCACGGTCACCTGACCAA 963
Qy 46 LysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeu 65
Db 964 CGATCAGAGCCTCTGATCATTCATTCAGACACTCTCCACAGCAGCCCGCAGCGTGGCAGTCTC 1023
Qy 66 LysAlaIleGlnGluGlnLeuIleAlaAsn-----ValHis 77
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Db 1024 CGGAGCAGAGAGAGAGAGAAATTTCTAAACCTGGGGCTGTCTCAACTCTCTGTAAAGCAT 1083
Qy 78 SerAsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArg 97
Db 1084 GCAGATGATCATACATATAAACAGTA-----GAAGAAGTTGTAGTTGAGAGA 1131
Qy 98 AsnGlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProVal 117
Db 1132 AATGAGAAA-----CAAGCACCCAGCTCTTCCA--- 1158
Qy 118 GlnGluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGln 137
Db 1159 -----GAACCAAGAGCTGTGTAT 1176
Qy 138 AsnGlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp 157
Db 1177 GCTCAAGTTGGACAAACAGATGTGGAT-----TTACCTGTCTAGTCCATCT 1221
Qy 158 AspAsp-----PheArgProGlyLeuLysAsp 166
Db 1222 GATGGCGTCTACCTAATTCAACTCATGAAGATGGATTCTCCGCCCCAGCATGAATTTG 1281
Qy 167 ThrLysLeuLeuLysThrLeuAlaIleGly----- 176
Db 1282 GTAAATTCAGAAAAGGAGATAGTGTGGGCCCTCGCCTGGCTGTGTGGAATGATGTGGA 1341
Qy 177 -----AspThrIleThrSerGlnGluLeuLeuAlaGlnAla 188
Db 1342 ATATTGTAGCTGGTGTCTAGAGATAGCCCTCGAGCCAAAGAGGCTTAGAAGAGGT 1401
Qy 189 GlnSerIleLeuAsnLysAsnHisProGlyTyrThrIleTyrGluArgAspSerIle 208
Db 1402 GATCAAAATTCACGGGTAACAATGTAGATTTCACA-----AACATC 1443
Qy 209 ValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGluPheThrTyr 228
Db 1444 ATAAAGAGAAGAACCGCTCTTTCTACTGACCTCCCTAAAGAGAGAGAGAGTACCATA 1503
Qy 229 ArgValLysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsnGluGlu 248
Db 1504 TTGGCTCAGAGAAGAAAGATGTTTATCGT-----CGC 1536
Qy 249 IleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGlyGluLysPro 268
Db 1537 ATTGTAGAAATCAGAT--GTGGGAGATCTTCTATAT-- 1572
Qy 269 TyrAspPropheAspArgSerHisLeuLysLeuPheThrIleLysTyrValAspValAsp 288
Db 1573 -----AGAACCACCTTTGAA----- 1587
Qy 289 ThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsnLeuAspPhe 308
Db 1587 ----- 1587
Qy 309 ArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPhe 328
Db 1588 -----TATGAAAAGGAATCTCCCTACGACTAGTTTAAACAAGAGAGGTGTTT 1638
Qy 329 GlyIleMetAspTyrThrLeuThrGlyLys-----ValGlu 340
Db 1639 CGTGTGTGGATACCTTGTAACATGGGAAACTAGGCTCTTGGCTCGCTATTTCGAATTCGC 1698
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1699 AAAAATCATAAAGAAGTAGAAGAGGCATCATCCCTAATAAGAACAGGGCTGAGCAGTTA 1758
Qy 361 GluAsnAlaSerTyrHisLeu 367
Db 1759 GCCAGTGTACAGTACACACTT 1779

RESULT 8
US-10-163-587B-3
; Sequence 3, Application US/10163587B
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; GENERAL INFORMATION:
; APPLICANT: OLIVEIRA, MARCOS
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10/163,587B
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/296,110
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 3859
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (160)..(3204)
US-10-163-587B-3
Alignment Scores:
Pred. No.: 0.0367 Length: 3859
Score: 105.00 Matches: 84
Percent Similarity: 35.66% Conservative: 49
Best Local Similarity: 22.52% Mismatches: 114
Query Match: 5.52% Indels: 127
DB: 6 Gaps: 16

US-09-940-235-2_COPY_16_383 (1-368) x US-10-163-587B-3 (1-3859)
Qy 35 GlyLysThrGluGlnGlyLeuSerProLysSerLysProPheAlaThrAspSerGly-Al 54
Db 1648 GGGAGTCAGCGGCTCGCTCTCCAAAAGAGCAAGGCGCCAGGTCAAGAGGAGGTATC 1707
Qy 54 aMetSerHisLysLeuGluLysAlaAspLeuLysAlaLeuGlnGluLeuLeuAl 74
Db 1708 AACAAATCTGAAAGAGAGAAATTAACCTCTAAAG-----GAGGAGCAGCTG- 1756
Qy 74 aAsnValHisSerAsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrI1 94
Db 1757 -----TGATCTCTGATTCTGGACTGGAA-CACTCTGGCGCATGT 1793
Qy 94 eThrAspArgAsnGlyLysValTyrPheAla- 104
Db 1794 CCTGGAGAAAGTGGGAGAGTCTTCAGTGCACCCCTGGCCCTGGTGACATCGTTAAAG 1853
Qy 105 -----AspLysAsp 107
Db 1854 AACCAACTCTCTACTACAAGCTGCAGCTTCTGGAGGACGACAAAGGAAACAGGTATTGGAT 1913
Qy 108 -----GlySerValThrLeuProThrGlnPr 116
Db 1914 ATTCAGTCTCTGGGCGGTGTGGGTACGGTGATCGGTAGCAACAACTGGAACAGATGCC 1973
Qy 116 oValGlnGluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProI1 136
Db 1974 GTCCAGGAGATGCCATGTGAGCATGATGATGATGATGATGATGATGATGATGATGATG 2027
Qy 136 eGlnAsnGlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnPr 156
Db 2028 GAACGCTTGGCACTCCAAAATTTTCAGCAAGTATCCCAAAAGTTTACCCCTGGAGAT 2087
Qy 156 oAsp-----AspAsp 165
Db 2088 TGACTATGGCAGGATGAAGAGGCGAGTGAAGAGTCAAGTAAATCTCGGCACCAAGTC 2147
Qy 166 -----AspThrLysLeuLeuLys 171
Db 2148 CAAGCTCCCAAGCAGTTCAGGACCTCATCAAGATGATCTTTGATGGGAAAGTATGAA 2207
Qy 171 sThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeu- 184
Db 2208 GAAAGCATGGTGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2267
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Qy 185 -----LeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThrIle 202
Db 2268 AAGCAGATCCAGCGCGCATCTCCATCTCAGTCAGTCCAGCAGCGGTCTCTCAGG 2327
Qy 202 rGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMe 222
Db 2328 CAGCAGCGACTCTCAGATCTCTCAAAATGCG-----TTTACACCTGATCCCCCA 2384
Qy 222 tAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsnLysL 242
Db 2385 CGACTTTGGGATG-----AAGAA 2402
Qy 242 sSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLys----- 258
Db 2403 GCCTCCGCTC-----CTGAACAATGCACACAGTGTGAGGCCCAAGTGAATGCT 2453
Qy 259 -----TyrTyrValLeuLysLysGly-----GluLys 267
Db 2454 TGACAACCTGCTGGACATCGAGGTGGCTTACAGTCTGCTCAGGGAGGCTCTCATGATAG 2513
Qy 267 sProTyrAspProPheAspArgSerHisLeuLysLeuPheThr-----IleLysTyrValAs 286
Db 2514 CAGCAAGGATCCCATCGATGTCAACTATGAGAAGCTCAAAACTGACATTAAGGTGTTGA 2573
Qy 286 pValAspThrAsnGlu-----LeuLeuLysSerGluGlnLeuLeuTh 300
Db 2574 CAGAGATTCTGAAGAGCGGAGATCATCAGGAGTATGTAGAACACTCATGCAACACC 2633
Qy 300 rAlaSerGluArgAsnLeuAspPheAspLeuTyr 312
Db 2634 ACACAGTCGTATGATCTTGAAGTATCATCGATATCTTT 2670

RESULT 9
US-60-615-573-13062
; Sequence 13062, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; TITLE OF INVENTION: Olansted, Stephen
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13062
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-60-615-573-13062

Alignment Scores:
Pred. No.: 0.00801 Length: 1248
Score: 104.50 Matches: 71
Percent Similarity: 37.13% Conservative: 53
Best Local Similarity: 21.26% Mismatches: 125
Query Match: 5.50% Indels: 85
DB: 8 Gaps: 16

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-13062 (1-1248)
Qy 58 LysLeuGluLysAlaAspLeuLeu-----LysAlaIleGlnGluGln 71
Db 274 AAAATAAATAAGGAGATAAAGTTTCAATTTTAAATCAAAAGTAAAGTATTAAACAATGAA 333
Qy 72 LeuIleAlaAsnValHisSerAsnAspTyrPheGluValIleAspPheAlaSerAsp 91
Db 334 CCAATTACTAGTATTAAATTCAGTGATGATTTTCAAAATGTTGTTGATATT----- 384
Qy 92 AlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAspLysAspGlySerValThr 111
```

Db 385 -----GATAAAATGTAGAAGTCTTTATCCCTAAAGATGAACACTACTGTTTCAT 432
Qy 112 LeuProThrGlnProValGlnGluPhe-----LeuLeuSerGlyHisValArgVal 128
Db 433 GATTCATTAATTTCAAGAGATTTTAAACAATGTGACAAACAGGGTGTTACTAAAGTA 492
Qy 129 ArgProTyrLysGlu-----LysProIleGlnAsnGlnAlaLys 141
Db 493 AACGAAGATAATGAAGTTTCCGAATGGATAGCAAAATCAATCTTAATGAATTTAGTGTAA 552
Qy 142 SerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPheArg 161
Db 553 ACGCTT-----TATTAGTTGTAAAGAGAACAACTAAAGAGATGCTGATTATAAA 603
Qy 162 ProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThr----- 178
Db 604 AATATATTAGTGAT-----AACTTACATCAATTTCTGATGTAGCTAAAGAA 651
Qy 179 ---IleThrSerGlnGluLeuLeuAlaGlnSerIleLeu----- 192
Db 652 CAATTAATTCACAGAGCTCAAGCTCAAGTGTAGATGTGATTATTAAGCCAGACTCA 711
Qy 193 AsnLysAsn-----HisProGlyTyrThr----- 200
Db 712 AACAAAGAACCTTGATTATATACAAATGCTTTAGCACATCAACACATTAGTTAGATTTA 771
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 772 TTGAATGATAGAAAATAAAAAAGCAACAATATAAATCAATCAACAACT----- 825
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 826 -----TCTAGTAGTCTAAAGATATTCAAAATTCACAAAC 861
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyr 260
Db 862 AAGTAAAGTAATTCGAATATAAATA-----ACATTGAATTTACAAGTGTAGTATGAA 918
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysIlePhe 280
Db 919 AAGAAAAGAAAGATAGTAGCAAGTCAAGATTCAAAAT-----AAATTAGTA 966
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 967 GATAAAGACAAACAAATACTCAAAATCTAAAGATTAAAAAGAAATACTAAAGAT 1026
Qy 301 AlaSerGluArgAsnLeuAspPheArgAsp----- 310
Db 1027 TCATCAAAATAATTTAGACTCCAAAGATAAAGAAAATATAAAGAAACATAAACA 1086
Qy 311 -----LeuTyrAspProArgAspLysAlaLysIleLeuTyrAsnAsnLeuAspAlaPhe 328
Db 1087 AAGAAACCACTGACAAACCTTACTAAAGAAAACCTATTACCATAACA----- 1134
Qy 329 GlyIleMetAsp-----TyrThrLeuThrGlyLysVal 339
Db 1135 GGTATGACAGATAATATTACGTACGTATGATGGGTAAATT 1176

RESULT 10
US-60-615-573-7856
; Sequence 7856, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084039 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7856

LENGTH: 2697
TYPE: DNA
ORGANISM: Streptococcus agalactiae
US-60-615-573-7856

Alignment Scores:
Pred. No.: 0.0493 Length: 2697
Score: 102.00 Matches: 66
Percent Similarity: 36.53% Conservative: 52
Best Local Similarity: 20.43% Mismatches: 99
Query Match: 5.37% Indels: 106
DB: 8 Gaps: 15

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-7856 (1-2697)

Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 772 GATTACCATGCAATTGTA---TTTTCAGCTTTGCTGCTATATTAAGACAAAGGGTGTAAAG 828
Qy 101 ValTyrPheAlaAsp-----LysAspGlySerVal 110
Db 829 ATTTATGTTACGATAAATTCAGAAACTTCTCGTATAGCGCTTAAGATAAACTGTT 888
Qy 111 ThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHisValArgValArgPro 130
Db 889 AAGATTGCTGAATTACCAATATGATGTACACATATTGATAGTTTATCTGTCGCT 948
Qy 131 TyrLysGlu---LysProIleGlnAsnGlnAlaLysSerValAspValGlu----- 146
Db 949 TTGAATGAGGTTAAACCTGTTGATAATATCTTGAATAATGATGACAAAGACATTAATCTC 1008
Qy 147 -----TyrThrValGlnPheThrProLeuAsnProAspAspPheArgProGly 163
Db 1009 AGCAAAACTTACCAATTAATAATACACCGACAAATCGTCTAGAGTTT----- 1059
Qy 164 LeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGlu 183
Db 1060 -----ACTATTAAATAACATAAC 1077
Qy 184 LeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThrIleTyrGlu 203
Db 1078 TCAAGTTTCAGAAATCATGACCCTTCAAGATGGAAGATGCCAGAAATGGTTGACAAA 1137
Qy 204 ArgAspSerIleValThrHisAspAsnAspIle-----PheArgThrIleLeu--- 220
Db 1138 AAAAGTTTCTTTGGATATAAACATATGACATGATGACATGATGATTAACACTATTGACTT 1197
Qy 221 ---ProMetAspGlnGluPheThrTyrArgVal----- 230
Db 1198 GGACGAAAGGATTCTGAATTTAAGGGACAACTTATTGCAAAAACCTGGAACAGTTGAATTA 1257
Qy 231 -----LysAsnArgGluGlnAlaTyrArgIleAsnLys----- 241
Db 1258 GATATGTTTTTCAACACATCTCAAGACCAGCTTCAATTTATTTAAAAAATATATACCTTATC 1317
Qy 242 LysSerGlyLeuAsnGluGluIleAsnAsn-----ThrAspLeu 254
Db 1318 CAAATGTTTCCAAATGAATTTGAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGT 1377
Qy 255 IleSerGluLysTyrTyrValLeuLys----- 263
Db 1378 CAGATAGATGACTACTATATTATAAAGATGCAATTAACCTTAAATTTAAATTAACCACT 1437
Qy 264 -----LysGlyGluLysProTyrAspProPheAspArgSer 275
Db 1438 GGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAA-----GATCCATAT-----AGT 1485
Qy 276 HisLeuLysLeuPheThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSer 295
Db 1486 CATCAGAAAGAGATATGACTAAA-----AAAGGT 1515
Qy 296 GluGlnLeuLeuThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArg 315
Db 1515 -----AAAGGT 1515

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Db 1516 GAACAGCTCAGTCATTCACAACTCAAGCCCAAT-----GAA 1548
Qy 316 AspLysAlaLysLeuLeuTyAsnAsnLeuAspAlaPheGlyIleMetAspTyThrLeu 335
Db 1549 AATACAGCAAAAGTAACCTTTGCTAAATATTGACTGGTGCATATTAGTAAGTTACTGTG 1608
Qy 336 ThrGlyLys 338
Db 1609 AATGCAAAA 1617

RESULT 11
US-10-856-118-1
; Sequence 1, Application US/10856118
; GENERAL INFORMATION:
; APPLICANT: Laidlaw, Stephen
; APPLICANT: Skinner, Mike
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Anderson, Richard
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 3742.1000-000
; CURRENT APPLICATION NUMBER: US/10/856,118
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: PCT/GB02/005411
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: GB0128733.3
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/334,649
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 266145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fowlpox virus genome
US-10-856-118-1

Alignment Scores:
Pred. No.: 48.5 Length: 266145
Score: 101.50 Matches: 73
Percent Similarity: 34.97% Conservative: 48
Best Local Similarity: 21.10% Mismatches: 90
Query Match: 5.34% Indels: 136
DB: 6 Gaps: 17

US-09-940-235-2_COPY_16_383 (1-368) x US-10-856-118-1 (1-266145)
Qy 69 GlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyThrPheGluValIleAspPhe 88
Db 134861 AAAGAGAGCTGTTTCTTAAATAAGATAAAATAGTATTATATGTTCTTGGCGGTAAG 134920
Qy 89 AlaSer---AspAlaThrIleThrAsp-----ArgAsnGlyLysValTy 102
Db 134921 AAAATATGAGAGCTATTATTAACAGATGCTACTAGCTTCTTAAATAATACAGAATCTAT 134980
Qy 103 PheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeu 122
Db 134981 TACTGTGATCATATAGATGCG-----GAATTTATGATG 135013
Qy 123 SerGlyHisValArgValArgProTyThrLysGluLysProIleGlnAsnGlnAlaLysSer 142
Db 135014 TGT-----TGTAGCAAGGGAATAT----- 135034
Qy 143 ValAspValGluTyThrValGlnPheThr-----ProLeuAsnProAspAsp 159
Db 135035 -----TATACTAATAACGGTACATGGCTTCTTACTAAGTAGTGCAGGAT 135082
Qy 160 PheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIle 179
Db 135083 -----ACTATTTCCTAGTATGCGTTGAC 135106
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Qy 180 ThrSerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTy 199
Db 135107 ACGCAAGAAAAATATTATACGACTATAAAGCGTATACAAATTTATCTCCCAACAGTAC 135166
Qy 200 ThrIleTyThrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIle 219
Db 135167 ACATCTTATCTTACAAAATTAATAGTATTAACTAAGCGTTGTGATTCTTTAGAGGACTT 135226
Qy 220 -----LeuProMetAspGlnGluPheThrTyArgVal-----LysAsn 232
Db 135227 TACGGAAATTTCTATAAATAAAGATAATTATATAGATACGAATTATTTACAGAAATTAAT 135286
Qy 233 ArgGluGlnAlaTyArg----- 238
Db 135287 AGAGAGAATGCATTCAGAAGCATAGCTCATAAAACTATAGCTTAAATTAATTTCTAATACC 135346
Qy 239 -----IleAsnLys 241
Db 135347 GATGAAAAATATAGATGAAATTTCTACTAACATAGATGTGATTTTGTGATTTTATAAACCCAC 135406
Qy 242 LysSerGlyLeuAsnGluLeuIleAsnAsnThrAsp----- 253
Db 135407 TATACATCGTTAAATGAAGATGCTTACAAATTTGAAGATTGCCGGATATACGTGTTAAG 135466
Qy 254 -----LeuIleSerGluLysTyThrValLeuLysLysGlyGluLysPro 268
Db 135467 GATTTCTTGGAGCTTATGTCGCTAGTAATGCTAC-----GAAGCTAAACAAACAG 135517
Qy 269 TyrAspProPheAspArgSerHisLeuLysLeuPheThr-----IleLysTyThrValAsp 286
Db 135518 TACGATC-TTGGATCGGATATATTACAAACATTTTACAAACGTTTATAAAGTACATAGAC 135575
Qy 287 Val-----AspThrAsnGluLeuLeuLysSerGluGlnLeu----- 299
Db 135576 GTAATTATGAAAAAGGAAAAAGAACGAATATATACTAAAAATGATAGAACTTTATAAATATA 135635
Qy 300 -----ThrAlaSerGluArgAsnLeu-- 306
Db 135636 GAAACATAAAATAAATACTATACTACATTTTATAAACTTCTAGGAATAGAACTTCTG 135695
Qy 307 -----AspPheArgAspLeuTyThrAspProArgAspLys 317
Db 135696 ATTCATATGCGTATTTGGGTATATTGGCGCTTCAGAAATTATATAT-----AGGTTTCG 135749
Qy 317 sAlaLysLeuLeuTy 322
Db 135750 AAGGAAGATCTTATTT 135765

RESULT 12
US-60-615-573-12450
; Sequence 12450, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12450
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-60-615-573-12450

Alignment Scores:
Pred. No.: 0.0159 Length: 945
Score: 100.50 Matches: 48
Percent Similarity: 36.12% Conservative: 34
Best Local Similarity: 21.15% Mismatches: 70
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Query Match: 5.23% Indels: 75
DB: 8 Gaps: 11

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-12450 (1-945)

Qy 195 AsnHisProGlyTyrThrIleTyrGluArgAspSerIleValThrHisAspAsnAsp 214
Db 13 AATCATGCAATCATTC-----AATCATTTGGAAATACAGGATTTAGAC 57

Qy 215 IlePhe-----ArgThrIleLeuProMet 222
Db 58 AATTTTCTTAAACCGGCTACTCTAATAGCGGTTGGACGACATCTGTGTGATATCT 117

Qy 223 AspGlnGluPheThrTyrArgValLys-----AsnArgGluGlnAla 236
Db 118 GATCAAAATTAAGTTTGTGCAATGACGATCGTTGGAATCTCAACCGAGACACGCT 177

Qy 237 TyrArgIleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSer 256
Db 178 CAAGCCCTTTCTAAATTTATGAGTGTAGAGCCCAAAATAAGACTTTGGGATATTCTTCAA 237

Qy 257 GluLysTyrTyrValLeuLysLysGlyGluLysProTyr----- 269
Db 238 ACRAAGTTTAAGCTAAGCACTTCAAGAAAGTTTATATTGAATATGACAAAGTGAAA 297

Qy 270 ---AspProPheAspArgSerHisLysLeuPheThrIleLysTyrValAspValAsp 288
Db 298 GCAGATAGTTGGATAGACGTAATATGCGT-----ATTGAATTTAAT 339

Qy 289 ThrAsnGluLeuLysSerGluGlnLeu----- 298
Db 340 CCAAAACAACTTACACGAGATGAATGATTGTTGTTAAACAAATATAATAAGCTACATG 399

Qy 299 -----LeuThrAlaSerGluArgAsnLeuAspPheArg-----Asp 310
Db 400 GAAGATGACGGTTTACAGATTAAGATTAGATTGACCTTTGATTGTTGAAGATGATTGAGTGAC 459

Qy 311 LeuTyrAspProArgAspLysAla-----LysLeuLeuTyrAsnAsnLeuAspAlaPhe 328
Db 460 TACTATGCAATGCTGATAAGCAGTAGTTAAGAAACTATTTT----- 501

Qy 329 GlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHis-----AspAsp 345
Db 502 -----TATGGTCGTAATGGTAAGCCAGAAACAAATATTTTGGCGTGAGAGAT 549

Qy 346 ThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAla----- 363
Db 550 AGTAATAGATTTATTAGAAATTTATAATAAAAGCAAGAAACGTAAGATAATATGCAGATGCT 609

Qy 364 -----SerTyrHisLeu 367
Db 610 GAAGTTATGCTGAACATTTA 630

RESULT 13
US-10-956-157-943
; Sequence 943 Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 943
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-943
Alignment Scores:
```

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Pred. No.: 0.039 Length: 1584
Score: 100.00 Matches: 88
Percent Similarity: 34.59% Conservative: 50
Best Local Similarity: 22.06% Mismatches: 129
Query Match: 5.26% Indels: 132
DB: 6 Gaps: 22

US-09-940-235-2_COPY_16_383 (1-368) x US-10-956-157-943 (1-1584)

Qy 27 LeuThrSerArgPro-----AlaHisGlyGly-----LysThrGluGln 39
Db 25 CTGACATCCCGTGTCTTCTTCTGTCGCCGGGGTCTTCTGCTGTGTCATGAAGACGTACCG 84

Qy 40 GlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeu 59
Db 85 GGTCTCTTACAGCAGAGCCAGAACTCCGGGCCCGGCGCCGCTGTGTGGCACCCTCTG 144

Qy 60 GluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsn 79
Db 145 GAGGAGCTC---TACACCAAGAAAGTTGTGCATCAGCTGACA----- 183

Qy 80 AspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGly 99
Db 184 -----CTTCAGGTCTTGAATTTGTGCGAGATCCGTGC----- 216

Qy 100 LysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGlu 119
Db 217 -----TTTGCCCAAGGAGATGCTCTCATTAAGCTTTATGAAAACTTTATCAGTGAA 267

Qy 120 PheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGln 139
Db 268 TTT-----GAACACAGGGTGAACCTTTGTCCCTCGTGGAATCATTTCTTCAT 315

Qy 140 AlalysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAsp 159
Db 316 GTAGTTAGACAGATGACTGATCTTAATGTGGCTCTTACTTTCTG-----GAAAG 366

Qy 160 PheArgProGlyLeuLysAspThrLys-----LeuLeuLysThr----- 172
Db 367 ACTCGTAGAAGGTGAAAAGTAGTAGTGAGCAGTGATCTGTGTAAACACAGCAATTGGA 426

Qy 173 -----LeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeuAlaGln 189
Db 427 GCTCTAAATTTAAACATCGGGACCTACAGGTTTACAAAGAAACAAATTGAAGATGTTGAA 486

Qy 190 SerIleLeuAsnLysAsnHisProGlyTyrThr----- 200
Db 487 GAAATGCTCAAC---AACCTTCTCTGTGTGACATCGGTTTCACAGTGTCTTCTATGATCTC 543

Qy 201 -----IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArg 217
Db 544 TCCAGTAAATACTATCAAAACAATCGGAAACACCGGCTCTCTACTACAAAGATGCTCTGCGG 603

Qy 218 ThrIle-----LeuProMetAspGlnGluPheThrTyrArgVal 230
Db 604 TTTTGGGCTGTGTTGACATCAAGGATCTACCAGTGTCTGAGCAG----- 648

Qy 231 LysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsn----- 246
Db 649 -----CAGGAGAGAGCCTTCGCTGGGGCTAGCAGGACTTCTCGCGCAGGGAGTTT 702

Qy 247 -----GluGluIleAsnAsnThrAsp----- 253
Db 703 AACTTTGGAGAACTCTCTATGACCCCTGTGTGGAGTCCCTGAGGATATCTGACCGGCAG 762

Qy 254 ---LeuIleSer-----GluLysTyrTyrValLeu 262
Db 763 TGGCTGATTGACACCCCTCTATGCTTCAACAGTGGCAAGTAGAGCGGTTCCAGACTCTG 822

Qy 263 LysLys-----GlyGluLysProTyrAspProPheAspArgSerHisLysLeuPhe 280
Db 823 AAGACTGCTGGGGCCAGCAGCT----- 846
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Qy 281 ThrileysTyrValAspValAspThrAsnGlu-----LeuLeuLysSerGluGlnLeu 298
Db 847 -----GATTAGCAGCTAATGAAGCCAGCTTCTGAGGAAATTCAGTTG 891
Qy 299 Leu-----ThralaSerGluArgAsnLeuAspPheArg 309
Db 892 TTGTGCTCATGGAGATGACTTTTACACAGCCTGCCAATCAGAGCAACTCATTCTTTGAA 951
Qy 310 AspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAlaPheGly 329
Db 952 GAAATT-----GCCAAAGTCTAAATCAGATGATGAGGTGGAGCTTCTG--- 999
Qy 330 IleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAspAspThrAsnArg 348
Db 1000 GTGATGAAGGCCCTTTTCGGTGGGCTGTGTGAAGCAGTATAGACGAGGTGGACAAA 1056

RESULT 14
US-10-163-587B-5
; Sequence 5, Application US/10163587B
; GENERAL INFORMATION:
; APPLICANT: OLIVEIRA, MARCOS
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10/163,587B
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/296,110
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 3845
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)..(3101)
US-10-163-587B-5

Alignment Scores:
Pred. No.: 0.144 Length: 3845
Score: 100.00 Matches: 75
Percent Similarity: 35.83% Conservative: 54
Best Local Similarity: 20.83% Mismatches: 129
Query Match: 5.26% Indels: 102
DB: 6 Gaps: 16

US-09-940-235-2_COPY_16_383 (1-368) x US-10-163-587B-5 (1-3845)

Qy 29 SerArgProAlaHisGlyGlyThrGluGlnGlyLeuSerProLysSerLysProPhe 48
Db 1569 TCCAAGAGCAAGGAGGCTGTCAAGAGGAGGAGGTGTCAACAAATCTGAAAGAGGATG 1628
Qy 49 Ala-----ThrAspSerGlyAla-----MetSer 56
Db 1629 AAATTAACCTGAAGGAGGAGGAGGAGGCTGTGATCTGCTGCTGGAACACTCTGCA 1688
Qy 57 HisLysLeuGluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnVal 76
Db 1689 CACGCTCTGGAGAAAGGTGGAGGTGTTCAGCCGCCACACTTGGCTGGTGACATGTTG 1748
Qy 77 HisSerAsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAsp 96
Db 1749 AAAGGAGCAACTCTTATTACAACTG-----CAGCTTCTGGAGGAC 1790
Qy 97 ArgAsnGlyLysValTyrPheAlaAspLysAsp-----Gly 108
Db 1791 GACAGGAGAGCAGGTACTGATCTTCGGTCTGGGCGGGGCGGACAGTTATCGGC 1850
Qy 109 SerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHisValArgVal 128
Db 1851 AGTAACAACTTGAGCAGATGCTCCCAAGAGGAGGAGGCTGTGTGAGCACTTTCATGAGCTG 1910
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Qy 129 ArgProTyrLysGluLysProIleGlnAsnGlnAlaLysSerValAspValGluTyrThr 148
Db 1911 -----TATGAAGAGAGACTGGGAATGCTGGCACTCGAAAAAAGTTCACAAAGTATCCC 1964
Qy 149 ValGlnPheThrProLeuAsnProAsp-----AspAsp----- 159
Db 1965 AAGAAGTTCTACCTCTCGAGATTGACTATGCCAGGAGCAAGAGCGAGCAAGAAAGCTG 2024
Qy 160 --PheArgProGlyLeuLys----- 165
Db 2025 ACGGTGAAGCCTGGCACCAGCTCGAAGCTGCCAAGCCAGTCGAGGAGCTCGTGGGGATG 2084
Qy 166 -----AspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGlu 183
Db 2085 ATCTTCGACGTGGAGAGCATGAAAAAGCGCTTGGTGGAGTACGAGATTACCTCCAGAA 2144
Qy 184 Leu-----LeuAlaGlnAlaGlnSerIleLeuAsnLys 194
Db 2145 ATGCCCTTTGGGAGAGCTGAGCAGAAAGGAGGAGTCCAGGCGCGCTACTCTATCTCTCAGCGAG 2204
Qy 195 AsnHisProGlyTyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAsp 214
Db 2205 GTCCAGCAGGCGAGTGTCTCAAGGCGAGCAGTGAATCCAGATCCTAGATCTCTCCAATCGC 2264
Qy 215 IlePheArgThrIleLeuProMetAspGlnGluPheThrTyrArgValLysAsnArgGlu 234
Db 2265 ---TCTACACTCTGATCCCCATGACTTTGGAATG----- 2297
Qy 235 GlnAlaTyrArgIleAsnLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeu 254
Db 2298 -----AAGAAGCCCGCCACTC-----CTGAACAACCGCAGACAGC 2330
Qy 255 IleSerGluLys-----TyrTyrVal 261
Db 2331 GTGAGGCGCAAGGTGGAGATGCTAGACAACCTCTGGACATCGAGTGGCCTATAGTCTT 2390
Qy 262 LeuLysLysGly-----GluLysProTyrAspProPheAspArgSerHisLeuLysLeu 279
Db 2391 CTCAGGGTGTGCTCTGACGACGACGAGCAAGGATCCATCGAGCTCACTCAGAGAACTC 2450
Qy 280 PheThr-----IleLysTyrValAspValAspThrAsnGlu-----Leu 292
Db 2451 AAAAAGTACATTAAAGTGTGGTGGACAGAGATTCTGAAGAGGCGGAGTGCATCAGGAAGTAC 2510
Qy 293 LeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyr 312
Db 2511 GTGAAGAACACTCATGCTATCCACGCAACACGCTATGACCTGGAAGTGCATATCTTTC 2570

RESULT 15
US-60-615-573-7919
; Sequence 7919, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7919
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-60-615-573-7919

Alignment Scores:
Pred. No.: 0.0567 Length: 1860
Score: 99.50 Matches: 70
Percent Similarity: 38.95% Conservative: 64
Best Local Similarity: 20.35% Mismatches: 117
```

Query Match: 5.23% Indels: 93
DB: 8 Gaps: 18

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-7919 (1-1860)

Qy 36 LysThrGlnGlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMet 55
:::|||||:::|
Db 544 GAAACAGATAGAGCCTTGGAAACGTCGGATCGAGCTGTATGTTGAAGAGCCAAACGATT 603
:::|||||:::|

Qy 56 SerHisLysLeuGluLysAlaAspLeuLeuLysAlaIleGlnGlu----- 70
|||:::|
Db 604 TCACAGCTATTACCATATTGAACAAGCTAAAGTCATTTATGAGAAAGTTTCATGGGATT 663
|||:::|

Qy 71 GlnLeuIleAlaAsn---ValHisSer----- 78
|||:::|
Db 664 CAAATTCCTCAGATCGTGTGCATCAAGCAATCCGTTTATCTGTTGCTATTGACAGAT 723
|||:::|

Qy 79 -----AsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThr 95
|||:::|
Db 724 CGATTCTTGGCGGATAAGGCTTTGATTGATCGATGAAGCG-----GCGACGATTGCT 777
|||:::|

Qy 96 AspArgAsnGlyLysValTyrPheAlaAspLysGlySerValThrLeuProThrGln 115
|||:::|
Db 778 TCAGTTGAAGGGAAGAAAGTAAAGTGACAGAAAAAGATATGCTCAAGTTTAAAGAGATAAA 837
|||:::|

Qy 116 -----ProValGlnGluPheLeuSerGlyHisValArgValArgProTyrLys 132
|||:::|
Db 838 ACGGAATTCCAGTCACTACTATCTTAAAGGGAGATCAAGNCGGTTAGAGGGTTTCANA 897
|||:::|

Qy 133 GluLysProIleGlnAsnGlnAlaLysSerValAsp-----ValGluTyrThrValGln 150
|||:::|
Db 898 GAAAGG---CTGATGAATCGAGTCAAAGGTCAAGAAGATGCCATTGAGCGCGTTGTAGAT 954
|||:::|

Qy 151 PheThrProLeuAsnProAspAspPheArgProGlyLeuLysAspThrLys----- 168
:::|
Db 955 GCGGTAACAGATT-----GCTCAAGCTCGTTTACAAAATGAAAAAGGCCG 999
|||:::|

Qy 169 LeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAla 188
|||:::|
Db 1000 CTTGCATCATCTCTTTCTCGGACCACTGGCGTGGGAAAAACAGAAATTAGCCAAAGCA 1059
|||:::|

Qy 189 GlnSerIleLeuAsnLysAsnHisProGlyTyrThrIleTyrGluArgAspSerSerIle 208
:::|
Db 1060 ATTGCA-----GAAGCACTTTTGTGATGATGAAGCTGCCATG 1095
|||:::|

Qy 209 ValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGluPheThrTyr 228
|||:::|
Db 1096 ATTCGTTTGTATATGTCGTAGTACAAA-----CAAAAAGAAGATGTGACTAAA 1143
|||:::|

Qy 229 ArgValLysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsnGluGlu 248
|||:::|
Db 1144 CTATCGGCAATCGT-----GCCACAAGATA-----AAGGACAATTGACTGAAGGA 1191
|||:::|

Qy 249 IleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGlyGluLysPro 268
:::|
Db 1192 GTAAAA-----CAGAAGCCT 1206
|||:::|

Qy 269 Tyr-----AspProPheAspArgSerHisLeuLysLeuPheThrIleLys 283
|||:::|
Db 1207 TATTGTCTCTGTTACTAGATGAGATTCAAAAAGCACACAGATGAGGTAATGGATCTTTTC 1266
|||:::|

Qy 284 TyrValAspValAspThrAsnGluLeuLysSer----- 295
|||:::|

Db 1267 TTGCAAGTGTAGATGATGTCGTTTAAACAGATAGTTCGGGTCGTTTATGATTAGCTTTAAA 1326
|||:::|

Qy 296 -----GluGlnLeuLeuThrAlaSerGlu 303
|||:::|

Db 1327 AACACATTGTGATTATGACCACCAATATTGGCGCTAAAAAAATCATCAATAAGTGGGAG 1386
|||:::|

Qy 304 ArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsn 323
|||:::|

Db 1387 TTGAAGGAAACCTTTAAAGATTAAACCGAT---CGAGATCGG---AAACAATTTGAAAAAG 1440
|||:::|

Qy 324 AsnLeuAspAla 327
:::|||||
Db 1441 TCGATGGACACT 1452

Search completed: November 6, 2004, 07:42:59
Job time : 210.055 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2004, 23:49:35 ; Search time 13.863 Seconds
(without alignments)
419.494 Million cell updates/sec

Title: US-09-940-235-2_COPY_16_383

Perfect score: 1901

Sequence: 1 SQLWSVAGTVEGTNODISL.....IITVMGKRPGENASYHLA 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 66696 seqs, 15802848 residues

Total number of hits satisfying chosen parameters: 66696

Minimum DB seq.length: 0

Maximum DB seq.length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pdp.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pdp.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pdp.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pdp.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pdp.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pdp.*
- 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pdp.*
- 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	134.5	7.1	1985	6 US-10-732-923-3351	Sequence 3351, Ap
2	121	6.4	2400	6 US-10-732-923-22508	Sequence 22508, A
3	107	5.6	1163	6 US-10-732-923-3296	Sequence 3296, Ap
4	105	5.5	1014	6 US-10-163-587B-4	Sequence 4, Appl
5	105	5.5	1014	6 US-10-163-587B-18	Sequence 18, Appl
6	105	5.5	1014	6 US-10-163-587B-37	Sequence 37, Appl
7	105	5.5	1014	6 US-10-163-587B-38	Sequence 38, Appl
8	105	5.5	1014	6 US-10-163-587B-39	Sequence 39, Appl
9	105	5.5	1014	6 US-10-163-587B-40	Sequence 40, Appl
10	104	5.5	1445	6 US-10-732-923-8160	Sequence 8160, Ap
11	103.5	5.4	1478	6 US-10-732-923-3353	Sequence 3353, Ap
12	103	5.4	921	6 US-10-732-923-3305	Sequence 3305, Ap
13	101	5.3	509	6 US-10-732-923-22708	Sequence 22708, A
14	100.5	5.3	1430	6 US-10-732-923-36	Sequence 36, Appl
15	100	5.3	1010	6 US-10-163-587B-6	Sequence 6, Appl
16	100	5.3	1501	6 US-10-732-923-22706	Sequence 22706, A
17	100	5.3	1553	6 US-10-732-923-22705	Sequence 22705, A
18	99.5	5.2	610	6 US-10-732-923-7214	Sequence 7214, Ap
19	99.5	5.2	639	6 US-10-732-923-7215	Sequence 7215, Ap
20	99.5	5.2	1087	6 US-10-732-923-8260	Sequence 8260, Ap
21	99	5.2	1089	6 US-10-732-923-8243	Sequence 8243, Ap
22	99	5.2	1555	6 US-10-732-923-22584	Sequence 22584, A
23	99	5.2	1765	1 PCT-US04-02460-1	Sequence 1, Appl
24	98.5	5.2	2497	6 US-10-732-923-8738	Sequence 8738, Ap
25	98.5	5.2	2497	6 US-10-732-923-8739	Sequence 8739, Ap

ALIGNMENTS

RESULT 1

US-10-732-923-3351

; Sequence 3351, Application US/10732923

; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10732,923

; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154

; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149

; SEQ ID NO 3351

; LENGTH: 1985

; TYPE: PRT

; ORGANISM: Plasmodium yoelii yoelii

; US-10-732-923-3351

Query Match 7.1%; Score 134.5; DB 6; Length 1985;

Best Local Similarity 23.2%; Pred. No. 0.0063; Mismatches 109; Indels 31; Gaps 10;

Matches 57; Conservative 49; Mismatches 109; Indels 31; Gaps 10;

QY 128 VRPKKEPIQQAQSDVVEYTVQFTPLNPDDEF--RPGKDKTKLLKTLAIGDTITTSQELL 185

Db 1222 IRRTERKSINYNNNLEINNSIQYIDSVINDFKPKFLKKN--NNLSNENFQOE-- 1277

QY 186 AQAOSILKNKHPGYTIYERDSSIVTHDN-DIPRTILPMDQEFYRYVKNREQAYRINKSG 244

Db 1278 -QGNNNNFKYPNDTY--DNSMDKNNRNTISNNSMKNITDYGNVNNDEPERENRQN 1333

QY 245 LNEENNTDLISEKYYVLKGEKPYDPDRSHLKLFTIKYVDVDTNELLKSQLLTASER 304

Db 1334 IS--NENDYYENKNDNKRKKYPPKPRANL-----EKDSYNNVANGNK---SER 1378

QY 305 NLDPRDLDPDRD---KAKLYNNLDAGIMDYTLTGKVEDNHDHDTNRIITVYMGKPEGE 361

Db 1379 NDNFNDLYNDNTVYKKEKYDNDNNYG--DHMYNNNDNNHNTKNGVYNNNNNGGY 1436

QY 362 NASYHL 367

Db 1437 NNSYNI 1442

RESULT 2

US-10-732-923-22508

; Sequence 22508, Application US/10732923

; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 22508
; LENGTH: 2400
; TYPE: PRT
; ORGANISM: Plasmodium falciparum 3D7
US-10-732-923-22508

Query Match 6.4%; Score 121; DB 6; Length 2400;
Best Local Similarity 20.5%; Pred. No. 0.11; Mismatches 43; Indels 110; Gaps 12;
Matches 63; Conservative

Qy 136 IQNQAK-----SDVVEYTVQFTPLNPDDDFRGLKDTKLLKTLAIGDRTITS 181
Db IKQKKIKMLNYTCTPINVRYNTSYIISSSELPVGGDIYEIKNNMTIPCDTIILSGSVTM 443
Qy 182 QELLAQAQS-----ILNKNHPGYTYIERDSSIVTHDND-----IF 216
Db 444 SEHMLTGESVPPIHKEQLPFEGNALINKNNKYESNDEKDDYLRYYNNHASINMIKRHLIE 503
Qy 217 RTILPMDQEP-----TY---RVKXREQAYRINKKSGLEENINNTDLI 255
Db 504 ETIGKKDREYKSNTHDLCMMNKLYINNTYDDVHMKNKMDYNNNNKKKKKINNLFV 563
Qy 256 SEKYVVLKGEKPYDPDRSHLKL-----TIKYVDVDTNELLKSEQLLTA 301
Db 564 KGTY--INSNDLLYD--DKIGVNIFEDDVNNMKHKFNQNNINYNKDTNNL----- 610
Qy 302 SERNLDRFDLYD-----PRDKALLYNNLDAGIMDYTLTG-----KVEDN 342
Db 611 -EYNNKHRYIYDCLLKKVEAISQKNKIYSNED---INKYMLYGGTYVLSLYNINKIKYN 666
Qy 343 HDDTNRII 350
Db 667 NKEENRII 674

RESULT 3

US-10-732-923-3296
; Sequence 3296, Application US/10732923

; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154

; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149

; SEQ ID NO 3296

; LENGTH: 1163

; TYPE: PRT

; ORGANISM: Clostridium acetobutylicum

US-10-732-923-3296

Query Match 5.6%; Score 107; DB 6; Length 1163;

Best Local Similarity 21.2%; Pred. No. 0.55; Mismatches 57; Indels 84; Gaps 14;

Matches 67; Conservative

Qy 16 QDISLKFEDLTSRPAHGGKTEOGLSPKSPFATDSDGAMSHKLEKADLLKAIQEQLIAN 75
Db 263 KOLMEKKDEIDLKKEARLGES-----SSKVKPYIDN---YENTLKQIDILK---EQIL-- 310
Qy 76 VHSNDDYFEIDFASDATITDRNGKVFADKDGSVTLPTQVQFLLSGHVVRPYKEKP 135
Db 311 --SRENTWKAISLEKE-----DMEKKLSIAKDNKEKALP-----KFMIKGHIILDAIREKD 359
Qy 136 -----IQNAQKSDVVEYTVQFTPLNPDDDFRGLKDTKLLKTLAIGDRTITSQEL 184

Db 360 LLDNIKLEKRLQKIEKLSLEAS-----NKEELIKQNIKIDSL-TLKIQNLESKIDN 412
Qy 185 LAQAQSIILNKNHPGYTYIERDSSIVTHDNDIFRTLPMQDEFTYRVKXREQAYRINKKSG 244
Db 413 LKVPPEYKKNINEG-----IFLRNTEKLEKHNKUG 444
Qy 245 LNEEINNTDL---ISEKYVVLKGEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLTA 301
Db 445 LDCDKFQVDFEKAQSKKEMLFNKLEE-----ERSKLDYTYKKLQDLN-KDFFPKDDVLLTF 498
Qy 302 SERNLDRFDLYDPRDK 317
Db 499 QEK-----LNDSRQK 508

RESULT 4

US-10-163-587B-4

; Sequence 4, Application US/10163587B

; GENERAL INFORMATION:

; APPLICANT: OLIVEIRA, MARCOS

; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING

; TITLE OF INVENTION: AGENTS

; FILE REFERENCE: 50229-306

; CURRENT APPLICATION NUMBER: US/10/163,587B

; CURRENT FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: 60/296,110

; PRIOR FILING DATE: 2001-06-07

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 4

; LENGTH: 1014

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-163-587B-4

Query Match

Best Local Similarity 5.5%; Score 105; DB 6; Length 1014;

Matches 77; Conservative 51; Mismatches 130; Indels 102; Gaps 16;

Qy 29 SRPAHGGKTEOGLSPKSPFA-----TDSGA--MSHKLEKADLLKAIQEQLIANV 76
Db 504 SKSKGQVKEEGINKSEKRMKLTLLKGAADVDPDSGLESAHVLEKGGKVFSAITGLVDIV 563
Qy 77 HSNDDYFEIDFASDATITDRNGKVFADK-----GSVTLPTQVQFLLSGHVVR 128
Db 564 KGTNSYKLL-----QLLEDDKENRYWIFRSWGRVGTWIGSNKLEQMPSEDAIEQFMKL 617
Qy 129 RPYKEKPIQNAQKSDVVEYTVQFTPLNP-----DD-----FRPGLK----- 165
Db 618 --YEKGTGNVHWSKNFTYKPKFYPLEIDYQDEEAVKLTIVNPGTKSLPKPVQDLIKW 675
Qy 166 --DTKLLKTLAIGDTITSQEL-----LAQAQSIILNKNHPGYTYIERDSSIVTHDND 214
Db 676 IFDVESMKAMVEYEDLQKMPGLKSKRQIAAYSIILSEVQQAQVSGSSDSQILDLSNR 735
Qy 215 IFRILPMQDEFTYRVKXREQAYRINKKSGLEENINNTDLISEK-----YV 261
Db 736 -FYTLIPHDFGM-----KKPPL---LNNADSVQAKVEMLDNLLDIEVAYS 777
Qy 262 LKKG-EKPYDPDRSHLKLFT-IKYVDVDTNE-----LLKSEQLLTASERNLDRFLY 312
Db 778 LRGSDDSSKDPIDVNYEKLKIDIKVDVDRDSEAEIRKYVKNTHATTHSAIDLEVIDIF 837

RESULT 5

US-10-163-587B-18

; Sequence 18, Application US/10163587B

; GENERAL INFORMATION:

; APPLICANT: OLIVEIRA, MARCOS

; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING

; TITLE OF INVENTION: AGENTS

; FILE REFERENCE: 50229-306


```
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3353
; LENGTH: 1478
; TYPE: PRT
; ORGANISM: Plasmodium yoelii yoelii
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1478)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-3353

Query Match      5.4%; Score 103.5; DB 6; Length 1478;
Best Local Similarity 20.0%; Pred. No. 1.5;
Matches 76; Conservative 71; Mismatches 138; Indels 95; Gaps 19;

QY 15 NODLSKFEFDLTSRPAHGKTE--QGLSPKSPKFPATDSGAMSHKLEKADLLKAI----- 68
DB 859 NSIINIINEIKTNKISNIEKSELKKNKLLKKKYNLSNDFLQNVEDVDKLLVKE 918
QY 69 --QOELIA-----NVHS--NDYFEVIDFASDATITDRNGKYVFADKDGSVTLTPQV 117
DB 919 SEQNELVITNEELKNLYKELNDEYNKINLIKONEYOIKNLQOELIEKNENKT-KTEEI 977
QY 118 QEFLLS-----CHVRVRPKPKPI-----QNAKSDVDVEYT 148
DB 978 NEFLKTDLDYLTSLSQANQSLTNLSENEKNKALKQLTENIYLNKQIEDKEENIEYL 1037
QY 149 VOFTPLNDDDFRPLGKD--TKLAKTLAIGDTITSQELLAQAQSLNKNHPGYTIYERDS 206
DB 1038 TQ--KIKSNDQVISLKEFNEMLIKKVETYSI--EELNRKEGNHTKGH-----IENS 1088
QY 207 SIVTHDNDIFRILPMDQEFYRVKNREQAYRI-----NKSGLNEEINWDLISEKYIV 261
DB 1089 TTELYDHRF-----YEDIDKNELGVSLENDNNNLKEE--CDMLKNDFYI 1134
QY 262 LKKGKPYDPDRSHLKLFTIKYVD--VD--TNELLKSEOLLTASER-----NL 306
DB 1135 L--SEKHLEEEITQKNDLPKYNDELDIKNDIIEKENLINERNKYKIKCIIDICFNK 1192
QY 307 DFRDLYDPRDKALYNNLD 326
DB 1193 DF-SIIDIREKIVAIFENDD 1211

RESULT 12
US-10-732-923-3305
; Sequence 3305, Application US/10732923.
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3305
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Fusobacterium nucleatum subsp. vincentii ATCC 49256
US-10-732-923-3305

Query Match      5.4%; Score 103; DB 6; Length 921;
Best Local Similarity 18.7%; Pred. No. 0.86;
Matches 84; Conservative 74; Mismatches 123; Indels 168; Gaps 20;

; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3305
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-732-923-22708

Query Match      5.3%; Score 101; DB 6; Length 509;
Best Local Similarity 19.2%; Pred. No. 0.56;
Matches 69; Conservative 59; Mismatches 115; Indels 116; Gaps 17;

QY 37 TEOGLSPKSPKFPATDSGAMSHKLEKADLLKATQOELIA---NVHSNDDYFEVIDFASDAT 93
DB 179 SHONINGNNKQYSSSSSLGIISNAPK---REISSRVISFKSKENKIYFNAPVPTS--S 232
QY 94 ITRDRNGKV--YFADKDGSVTLTPQVQOEFLLSG-----HVRVRPKYKEKPIQNAKSV 143
DB 233 LIEELGQIEYIFSDKTGTLTCNIMEFRKCAINGISYKGLTEIKRNILKKNLKLE-----I 287
QY 144 DVEYTVQFTPLNP-----DDDFRPLGKD-----TKLAKTLAIGDTITSQELLAQAQ 189
DB 288 PVEPTMKFKKTPHVNIIIDNDIINHLKDPNHNHVNLIINFELHLAINHAV----- 337
QY 190 SILNKNHPGYTIYERDS-----SIVT-----HNDIFRILPMDQ-----E 225
DB 338 -ICEKDKGVTTYSYSSSPDEEALVNAAKHFDITFLYRREGKYGISIFGKIYEDTLTATIE 396
QY 226 FTYRVKNREQAYRI-----NKSGLNEEINWDLISEKYIVLKKGKPK----- 268
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Db 397 FTSKRMSVICRIPVINPDYHPTDAKSNMCKQNMND----DHLVVGKNEKEETDD 452
Qy 269 ---YDPFDRSHLKLFTIKYVDVDNELLKSQLLTASERNLDFRDYDPRDKAKLLYNN 324
Db 453 LNVYPPKKEAHSKU-----NNN-----NNNRIDNLDYDKNNFNIIYNH 492

RESULT 14
US-10-797-821-36
; Sequence 36, Application US/10797821
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REFERENCE: 25669-020
; CURRENT APPLICATION NUMBER: US/10/797,821
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 10/383,930
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/363,209
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 09/290,049
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 60/081,550
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/115,142
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 36
; LENGTH: 1430
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-36

Query Match 5.3%; Score 100.5; DB 6; Length 1430;
Best Local Similarity 20.5%; Pred. No. 2.5;
Matches 102; Conservative 77; Mismatches 163; Indels 155; Gaps 26;

Qy 6 SVAGTVESTNQDISLKEFEID--LTSRPAHGKTEQGLSPKSPKFPATDSGAMSHKLEKAD 63
Db 91 STSITKETPSQNIITQANSDDKTNTKSEEAQTESEERTKQSEEAQTITASSQALTAQAE 150
Qy 64 LLKAIQEOILANVHNSDDYFVIDPASDATITDRNGKVFADKQSGVTLTPQVQEFLLS 123
Db 151 LTK--QRQTAQENKNP-----VDLAAIPNVKQIDGKYIYIGSDG-----QPKKNFALT 197
Qy 124 GHVRVPYKEK-----PIQNOAKSVDEVYTVQFTPLN----- 155
Db 198 VNNKLVYDKNKGALTDTSQYQFKQGLTKLNDYTPHNQIVNFENTSLETIDNYYVTADSW 257
Qy 156 ---PDD-----DPRPGL-----KDTKLL-----KTLAIGDTIT---SQE 183
Db 258 YRPDKILKNGKWTASSESDLRPLMSWPKQTOIAYLVNMQOGLGTGENYTADSSQE 317
Qy 184 ---LLAQ-----QSILN-----KNHPGYTIY-EROSIVTHNDIPIRT 218
Db 318 SLNLAAQTQVVKIETKISQTOQTOWLRDIINSFVKTPQNMNSQTESDTSAGEKDHLOGGA 377
Qy 219 ILPMDQBEFT-----YRVKNR-----EQAYRINKKSG-----LNBEINNTDLISEK-- 258
Db 378 LLYSNSDKTAVANSYDRLLNTPTSQTGPKFYFEDNSSGGYDFLLANDIDNSNPVVQAEQ 437
Qy 259 ----YYVLKKG-----EKPYDPFDRSHLKLFTIKYVDVD-----TNELKSEQLLTASERN- 305
Db 438 LNWHLHLMNYGSIIVANDPEANFD--GVRVDAVDVNVADLLQIASDYLKAHYGVDKSEKNA 495
Qy 306 ---LDPRDLYDPRDK-----AKLLYNNLDFAFGIMDYTYLTGKVEDNHDNTRT----- 349
Db 496 INHLSILEAWSNDPQYNKOTKGAQLPIDNKLRLSL--YALTRPLEKDAKNKNEIRSGLE 554
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Qy 350 ---ITVYMGR-PEGENA 363
Db 555 PVITNSLNNRSGAEGKNS 571

RESULT 15
US-10-163-587B-6
; Sequence 6, Application US/10163587B
; GENERAL INFORMATION:
; APPLICANT: OLIVEIRA, MARCOS
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10/163,587B
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/296,110
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 6
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-163-587B-6

Query Match 5.3%; Score 100; DB 6; Length 1010;
Best Local Similarity 20.8%; Pred. No. 1.7;
Matches 75; Conservative 54; Mismatches 129; Indels 102; Gaps 16;

Qy 29 SRPAHGKTEQGLSPKSPFA-----TDSGA--MSHKLEKADLLKAIQEOILANV 76
Db 500 SKKSGKAVKEGKVNKSEKRMKLTLLKGGAAVDPSGLEHSAHVLEKGGKVFSAATLGLVDIV 559
Qy 77 HSNDDYFEVIDPASDATITDRNGKVFADKD-----GSVTLTPQVQEFLLSGHVRV 128
Db 560 KGTNSYKKL-----QLLEDDKESRYWIFRSWGRVGTIGSNKLSQMPSEKDAVEHFMKL 613
Qy 129 RPYKEKPIQNOAKSVDEVYTVQFTPLNPD---DD-----PRPGLK----- 165
Db 614 --YEKTNHNSKNTFYKPKFPYLEIDYQDEEAVKKLTVKPGTKSKLPKPVQELVGM 671
Qy 166 --DTKLLKTLAIGDTITSQEL-----LAQASILNKNHPGYTIYERDSIVTHDND 214
Db 672 IFDVESMKALVEVEIDLQKMPGLKLSRRQIAOAYSILSEVQOAVSQSSSQSILDSNR 731
Qy 215 IFRILPMDQBEFTYRVKREQAYRINKKSGLNBEINNTDLISEK-----YYV 261
Db 732 -FYLIPHDFGM-----KKPPL---LNNADSVQAKVEMLDNLLDIEVAYSL 773
Qy 262 LKKG--EKPYDPFDRSHLKLFT-IKYVDVDTNE-----LLKSEQLLTASERNLDFRDLY 312
Db 774 LRGSDDSSKDPIDVNYEKLKTDIKVDRDSEAEVIRKYVKNTHATTHNAYDLEVIDIF 833

Search completed: November 4, 2004, 00:11:48
Job time : 15.863 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:38:12 ; Search time 34.0925 Seconds
(without alignments)
747.335 Million cell updates/sec

Title: US-09-940-235-4_COPY_150_259

Perfect score: 627

Sequence: 1 PIAEKCFDHAAGTSYVVGET.....ERHTSVQTSGGSPFTDVR 110

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 693957 seqs, 115811272 residues

Total number of hits satisfying chosen parameters: 1387914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cg2_1/USPTO.spool_P/US09940235/runat_03112004_174040_11339/app_query.fasta_1.1045
-DB=Pending Patents NA New -QFMT=fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09940235@cgn_11_480@runat_03112004_174040_11339
-NCFU=6 -ICFU=3 -NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=130 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA New.*

1: /cg2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
2: /cg2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cg2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cg2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cg2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cg2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /cg2_6/ptodata/2/pna/US11_NEW_COMB.seq.*
8: /cg2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	627	100.0	2127	6	US-10-956-157-4288
2	627	100.0	2402	1	PCT-US04-31524-364
3	627	100.0	7677	6	US-10-956-157-4995
4	627	100.0	7680	6	US-10-948-737-4446
5	627	100.0	7912	1	PCT-US04-31524-366
6	627	100.0	8272	1	PCT-US04-31524-370
7	627	100.0	8374	1	PCT-US04-31524-374
8	627	100.0	8449	1	PCT-US04-31524-190
9	627	100.0	8647	1	PCT-US04-31524-368
10	627	100.0	8815	1	PCT-US04-31524-372

11	627	100.0	8815	6	US-10-868-577A-62	Sequence 62, Appl	
12	218	34.8	600	6	US-10-956-160-215929	Sequence 215929, Ap	
13	218	34.8	1567	6	US-10-956-160-5822	Sequence 5822, Ap	
14	213	34.0	600	6	US-10-956-157-9521	Sequence 9521, Ap	
15	213	34.0	607	6	US-10-948-737-12304	Sequence 12304, A	
16	213	34.0	1400	6	US-10-956-157-10230	Sequence 10230, A	
17	213	34.0	2384	6	US-10-956-157-4286	Sequence 4286, Ap	
18	201	32.1	600	6	US-10-956-157-9523	Sequence 9523, Ap	
19	165	26.3	588	6	US-10-956-157-4994	Sequence 4994, Ap	
20	165	26.3	588	6	US-10-956-157-10229	Sequence 10229, A	
21	165	26.3	1241	6	US-10-956-157-234	Sequence 234, App	
22	165	26.3	1241	6	US-10-956-157-5469	Sequence 5469, Ap	
23	119.5	19.1	600	6	US-10-956-160-215928	Sequence 215928, Ap	
24	119.5	19.1	794	6	US-10-956-160-5821	Sequence 5821, Ap	
c	89	14.2	7017	6	US-10-956-157-413	Sequence 413, App	
26	81	12.9	407	6	US-10-964-549-799	Sequence 799, App	
27	76.5	12.2	609	6	US-10-948-737-3916	Sequence 3916, Ap	
c	28	74	11.8	565	6	US-10-948-737-7910	Sequence 7910, Ap
c	29	73	11.6	327	6	US-10-948-737-4102	Sequence 4102, Ap
c	30	73	11.6	328	6	US-10-948-737-4224	Sequence 4224, Ap
c	31	73	11.6	385	6	US-10-948-737-4808	Sequence 4808, Ap
c	32	73	11.6	421	6	US-10-948-737-775	Sequence 775, App
c	33	73	11.6	446	6	US-10-948-737-1057	Sequence 1057, App
c	34	73	11.6	448	6	US-10-220-366A-13515	Sequence 13515, A
c	35	73	11.6	499	6	US-10-948-737-1099	Sequence 1099, Ap
c	36	72	11.5	420	6	US-10-220-366A-13860	Sequence 13860, A
c	37	72	11.5	1186	8	US-60-613-292-977	Sequence 977, App
c	38	72	11.5	4743	6	US-10-956-157-4104	Sequence 4104, Ap
c	39	71.5	11.4	2808	6	US-10-956-157-1543	Sequence 1543, Ap
c	40	71.5	11.4	6761	6	US-10-960-275-1	Sequence 1, Appl1
c	41	71.5	11.4	7561	6	US-10-967-702-21	Sequence 21, Appl
c	42	71	11.3	1082	6	US-10-486-706-211	Sequence 211, App
c	43	71	11.3	1400	6	US-10-956-157-6117	Sequence 6117, App
c	44	71	11.3	2914	6	US-10-956-157-882	Sequence 882, App
c	45	70.5	11.2	660	8	US-60-615-573-18478	Sequence 18478, A

ALIGNMENTS

RESULT 1
US-10-956-157-4288
; Sequence 4286, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4288
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4288

Alignment Scores:
Pred. No.: 1.96e-63 Length: 2127
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-157-4288 (1-2127)

Qy	1	ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr	20
Db	597	CCCATAGCTGAGAGTGTGTTTTCATCTGCTGGACTTCCTATGCTGCGGAGAACG	656
Qy	21	TrpGluLysProTyrGlnGlyTrpMetValAspCysThrCysLeuGlyGluGlySer	40

Db 657 TGGGAGAAGCCCTACCAAGGCTGGATGATGTAGATTGTTCTGCTGGGAGAAGGCG 716
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 717 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACCATGATCAGGACACAAAGGACATCCTAT 776
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysileCys 80
Db 777 AGAATTGGAGACACTGGAGCAAGAGGATTAATCGAGAAACCTGCTCCAGTGATCTGC 836
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 837 ACAGCAACGCCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGACAGACCATCG 896
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 897 AGCGGATCTGGCCCTTCACCGATGTTGCT 926

RESULT 2

PCT-US04-31524-364
; Sequence 364, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 364
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-364

Alignment Scores:

Pred. No.: 2,31e-63 Length: 2402
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_copy_150_259 (1-110) x PCT-US04-31524-364 (1-2402)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 807 CCCATAGCTGAGAAGTGTGTTGATCATGCTCTGGGACTTCTCTATGTTGGTGGGAGAAGCG 866
Qy 21 TrpGluLysProTyrGlnGlyTrpMetValAspCysThrCysLeuGlyGlySer 40
Db 867 TGGGAGAAGCCCTACCAAGGCTGGATGATGTAGATTGTTCTGCTGGGAGAAGGCG 926
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 927 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACCATGATCAGGACACAAAGGACATCCTAT 986
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysileCys 80
Db 987 AGAATTGGAGACACTGGAGCAAGAGGATTAATCGAGAAACCTGCTCCAGTGATCTGC 1046
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 1047 ACAGCAACGCCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGACAGACCATCG 1106
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 1107 AGCGGATCTGGCCCTTCACCGATGTTGCT 1136

RESULT 3

US-10-956-157-4995
; Sequence 4995, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4995
; LENGTH: 7677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4995

Alignment Scores:

Pred. No.: 1.06e-62 Length: 7677
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-157-4995 (1-7677)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 461 CCCATAGCTGAGAAGTGTGTTGATCATGCTCTGGGACTTCTCTATGTTGGTGGGAGAAGCG 520
Qy 21 TrpGluLysProTyrGlnGlyTrpMetValAspCysThrCysLeuGlyGlySer 40
Db 521 TGGGAGAAGCCCTACCAAGGCTGGATGATGTAGATTGTTCTGCTGGGAGAAGGCG 580
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 581 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACCATGATCAGGACACAAAGGACATCCTAT 640
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysileCys 80
Db 641 AGAATTGGAGACACTGGAGCAAGAGGATTAATCGAGGAAACCTGCTCCAGTGATCTGC 700
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 701 ACAGCAACGCCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGACAGACCATCG 760
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 761 AGCGGATCTGGCCCTTCACCGATGTTGCT 790

RESULT 4

US-10-948-737-4446
; Sequence 4446, Application US/10948737
; GENERAL INFORMATION:
; APPLICANT: CHAN, VIVIEN W.
; APPLICANT: ESCOBEDO, JAIME
; APPLICANT: GARCIA, PABLO DOMINGUEZ
; APPLICANT: HANSEN, RHONDA
; APPLICANT: KAUFMANN, JOERG
; APPLICANT: KENNEDY, GIULIA C.
; APPLICANT: LAMSON, GEORGE
; APPLICANT: MOLER, EDWARD J.
; APPLICANT: RANDAZZO, FILIPPO
; APPLICANT: REINHARD, CHRISTOPH
; APPLICANT: SUDDUTH-KLINGER, JULIE
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 2300-21987
; CURRENT APPLICATION NUMBER: US/10/948,737

; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 10/616,900
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: 09/872,850
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,871
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 10/081,519
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,959
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/310,673
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/336,613
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US03/00657
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/345,637
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: 10/081,124
; PRIOR FILING DATE: 2002-02-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13996
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4446
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-737-4446

Alignment Scores:
Pred. No.: 1,06e-62 Length: 7680
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-948-737-4446 (1-7680)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaLaGlyThrSerTyrValValGlyGluThr 20
Db 461 CCCATAGCTGAGAAGTGTTCATCATGCTGCTGGACTTCCTATGTTGCTGGAGAAACG 520
Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db 521 TGGGAGAGCCCTACCAAGGCTGGATGATGTTAGTATTGTTACTTGGCTGGAGAGGCAGC 580
Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 581 GGACGCATCATCTTGCACCTCTAGAAATAGATGCAACGATCAGGACACCAAGGACATCCTAT 640
Qy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysIleCys 80
Db 641 AGAATTGGAGACACCTGGAGCAAGAGATATATCGAGAAACCTGCTCCAGTGCATCTGC 700
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 701 ACAGCAACGCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGCAGACACATCG 760
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 761 AGCGGATCTGCCCTTCACCGATGTTTCTGT 790

RESULT 5
PCT-US04-31524-366
; Sequence 366, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01

; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366
; LENGTH: 7912
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-366

Alignment Scores:
Pred. No.: 1.11e-62 Length: 7912
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x PCT-US04-31524-366 (1-7912)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaLaGlyThrSerTyrValValGlyGluThr 20
Db 807 CCCATAGCTGAGAAGTGTTCATCATGCTGCTGGACTTCCTATGTTGCTGGAGAAACG 866
Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db 867 TGGGAGAGCCCTACCAAGGCTGGATGATGTTAGTATTGTTACTTGGCTGGAGAGGCAGC 926
Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 927 GGACGCATCATCTTGCACCTCTAGAAATAGATGCAACGATCAGGACACCAAGGACATCCTAT 986
Qy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysIleCys 80
Db 987 AGAATTGGAGACACCTGGAGCAAGAGATATATCGAGAAACCTGCTCCAGTGCATCTGC 1046
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 1047 ACAGCAACGCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGCAGACACATCG 1106
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 1107 AGCGGATCTGCCCTTCACCGATGTTTCTGT 1136

RESULT 6
PCT-US04-31524-370
; Sequence 370, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 8272
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-370

Alignment Scores:
Pred. No.: 1.17e-62 Length: 8272
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0


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; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 8647
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-368

Alignment Scores:
Pred. No.: 1,24e-62 Length: 8647
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x PCT-US04-31524-368 (1-8647)

Qy 1 ProtleAlaGluLysCysPheAspHisalaAlaGlyThrSerTyrValValGlyGluThr 20
Db 807 CCCATAGCTGAGAAGTGTGTTTGGATCATGCTCTGGGACTTCTTATGTTGGTGGAGAAACG 866

Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGlySer 40
Db 867 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGTATTGTTACTTGCCTGGGAGAAGGCACG 926

Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 927 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAAGCATCAGGACACAAAGGACATCCTAT 986

Qy 61 ArgileGlyAspThrTrpSerLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 987 AGAATTGGAGACACCTGGAGCAAGAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC 1046

Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrSer 100
Db 1047 ACAGGCAACGCCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGAGACCATCG 1106

Qy 101 SerGlySerGlyProPheThrAspValArg 110
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RESULT 10
; Sequence 62, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alicao et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 8815
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-577A-62

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Pred. No.: 1,28e-62 Length: 8815
Score: 627.00 Matches: 110
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-868-577A-62 (1-8815)

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Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 927 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAAGCATCAGGACACAAAGGACATCCTAT 986

Qy 61 ArgileGlyAspThrTrpSerLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
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Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrSer 100
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Qy 101 SerGlySerGlyProPheThrAspValArg 110
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PCT-US04-31524-372
; Sequence 372, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 8815
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-372

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RESULT 12
US-10-956-160-215929
; Sequence 215929, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215929
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-215929
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Score: 218.00 Matches: 35
Percent Similarity: 55.91% Conservativeness: 17
Best Local Similarity: 37.63% Mismatches: 39
Query Match: 34.77% Indels: 2
Gaps: 6
DB: 1

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; Sequence 9521, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9521
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9521
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Score: 213.00 Matches: 35
Percent Similarity: 55.91% Conservativeness: 17
Best Local Similarity: 37.63% Mismatches: 39
Query Match: 33.97% Indels: 2
Gaps: 6
DB: 1

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Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db 100 TGGGAACGAATGCTCTGAATCAGGCTTTAAACTGTTGTCACGATGCTTAGGCTTTGGAAGT 159

RESULT 13
US-10-956-160-5822
; Sequence 5822, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5822
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-5822
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Pred. No.: 5,09e-16 Length: 1567
Score: 218.00 Matches: 35
Percent Similarity: 55.91% Conservativeness: 17
Best Local Similarity: 37.63% Mismatches: 39
Query Match: 34.77% Indels: 2
Gaps: 6
DB: 1

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Db 1300 TGGGAGCGGTGCTCTGAATCTGGCTTTAAGCTCTCGTCCAGTGTAGGCTTTGGCAGT 1359
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 1360 GGTCAATTCAGATGTGACTCATCTAAATGGTGCCATGATAATGGT-----GTGAACATAC 1413
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysileCys 80
Db 1414 AAGATTGGCGAAGATGGGATCGTCAGGGGGAGAAATTCAGTGTGATCTCTCAT 1512
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHis 93
Db 1474 CTTGGAATGAAAGAGAGAAATTCAGTGTGATCTCTCAT 1512

RESULT 14
US-10-956-157-9521
; Sequence 9521, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9521
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9521
Alignment Scores:
Pred. No.: 5,5e-16 Length: 600
Score: 213.00 Matches: 35
Percent Similarity: 55.91% Conservativeness: 17
Best Local Similarity: 37.63% Mismatches: 39
Query Match: 33.97% Indels: 2
Gaps: 6
DB: 1

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-157-9521 (1-600)
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Db 40 CCTACGATGACTCGTGTCTTGCACCCCTACACAGTTTCCCATTAATGCCGTTGGAGATGAG 99
Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db 100 TGGGAACGAATGCTCTGAATCAGGCTTTAAACTGTTGTCACGATGCTTAGGCTTTGGAAGT 159
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11	600	100.0	7679	62	US-10-831-704-38
12	600	100.0	7680	2	PCT-US02-02176-1216
13	600	100.0	7680	2	PCT-US02-10824-60
14	600	100.0	7680	2	PCT-US02-14877A-654
15	600	100.0	7680	2	PCT-US02-15982-75
16	600	100.0	7680	2	PCT-US02-15982A-75
17	600	100.0	7680	2	PCT-US02-18638A-63
18	600	100.0	7680	2	PCT-US04-07268-79
19	600	100.0	7680	2	PCT-US04-15421-122
20	600	100.0	7680	15	US-09-053-375B-1319
21	600	100.0	7680	21	US-09-440-302A-1117
22	600	100.0	7680	21	US-09-440-302B-1117
23	600	100.0	7680	21	US-09-442-589B-1143
24	600	100.0	7680	24	US-09-543-679A-2698
25	600	100.0	7680	43	US-09-964-824C-574
26	600	100.0	7680	43	US-09-964-824C-574
27	600	100.0	7680	48	US-10-171-311-63
28	600	100.0	7680	48	US-10-182-936A-75
29	600	100.0	7680	49	US-10-219-051B-9261
30	600	100.0	7680	49	US-10-236-031B-69
31	600	100.0	7680	49	US-10-240-851-75
32	600	100.0	7680	50	US-10-278-698-88
33	600	100.0	7680	50	US-10-278-698-603
34	600	100.0	7680	52	US-10-374-979-75
35	600	100.0	7680	54	US-10-470-050-1216
36	600	100.0	7680	54	US-10-477-173-654
37	600	100.0	7680	54	US-10-477-238A-654
38	600	100.0	7680	57	US-10-641-643-1289

39 600 100.0 7680 57 US-10-680-287A-654
 40 600 100.0 7680 60 US-10-717-597-222
 41 600 100.0 7680 61 US-10-788-792-79
 42 600 100.0 7680 62 US-10-843-641A-5877
 43 600 100.0 7680 95 US-60-290-071-75
 44 600 100.0 7680 108 US-60-427-982-222
 45 600 100.0 7680 111 US-60-459-782-222

ALIGNMENTS

RESULT 1

US-09-471-349-3
 ; Sequence 3, Application US/09471349
 ; GENERAL INFORMATION:
 ; APPLICANT: Sahni, Girish
 ; APPLICANT: Kumar, Rajesh
 ; APPLICANT: Roy, Chaiti
 ; APPLICANT: Rajagopal, Kammar
 ; APPLICANT: Nihalani, Deepak
 ; APPLICANT: Sundaram, Vasudha
 ; APPLICANT: Yadav, Mahavir
 ; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
 ; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
 ; FILE REFERENCE: 07064/009001
 ; CURRENT APPLICATION NUMBER: US/09/471,349
 ; CURRENT FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
 ; PRIOR FILING DATE: 1998-12-24
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 777
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(777)
 US-09-471-349-3

Alignment Scores:
 Pred. No.: 1.09e-59 Length: 777
 Score: 600.00 Matches: 106
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-09-471-349-3 (1-777)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
 Db 1 CAGGCTCAGCAATGGTTTCAGCCCGGTCGCTGTCAGTCAAGCAAGCCCGGT 60
 Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnTrpGluArgThrTyrLeuGly 40
 Db 61 TGTATGATCAATGAAACACATATCAGATAATCAACAGTGGGAGCGGACCTACCTAGGT 120
 Qy 41 AsnValLeuValCysThrCysTyrGlySerArgGlyPheAsnCysGluSerLysPro 60
 Db 121 AATGTTGGTTTGTACTTGTATGGAGGAGCCGAGGTTTAACTCGGAAGTAAACCT 180
 Qy 61 GluAlaGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
 Db 181 GAAGCTGAAGAGACTTGTCTTTCACAAAGTACACTTACGAGTGGGTGACACT 240
 Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
 Db 241 TATGAGCGTCTCAAGACTCCATGATCTGGGACTGATCTGATCGGGGCTGGGAGGG 300
 Qy 101 ArgIleSerCysThrIle 106

```

; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(777)
US-10-631-558-3

Alignment Scores:
Pred. No.: 1,09e-59 Length: 777
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-631-558-3 (1-777)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1 CAGGCTCAGCAAAATGGTTTCAGCCCCAGTCCCGGTGGCTGTCTCAGTCAAAAGCAAGCCCGGT 60

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 61 TGTATTGACAAATGGAAACAACTATCATGATAAATCAACAGTGGGAGCGGACCTTACTTAGT 120

Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 121 AATGTGTGTGTTTGTACTTGTATTGGAGGAAGCCGAGGTTTAACTCGGAAGTAAACCT 180

Qy 61 GluAlaGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 181 GAAGCTGAAGAGACTTGCTTTGACAGTACACTGGGAACACTTACCAGAGTGGGTGACACT 240

Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 241 TATGAGCGTCTTAAAGACTCCATGATCTGGGACTGTACCTACCTCGGCGGTGGGCGAGGG 300

Qy 101 ArgIleSerCysThrIle 106
Db 301 AGAATAAGCTGTACCATC 318

RESULT 4
US-09-471-349-10
; Sequence 10, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara

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; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-471-349-10

Alignment Scores:
Pred. No.: 2,78e-59 Length: 1661
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-09-471-349-10 (1-1661)
Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1341 CAGCGCAGCAAAATGGTTTCAGCCCGTCCCGTGGTGTTCAGTCAAGCAAGCCCGGT 1400
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgTyrTyrLeuGly 40
Db 1401 TGTATGACAAATGGAACACATATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGT 1460
Qy 41 AsnValLeuValCysThrCysTyrGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 1461 AATGTGTTGGTTTGTACTTGTATCGAGGAAGCGAGGTTTAACTGCGAAAGTAAACCT 1520
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 1521 GAAGCTGAAGAGACTTGTCTTTGACAAGTACACTGGGACACTTACCGAGTGGTGACACT 1580
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyValaGlyArgGly 100
Db 1581 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACTGCTCGGGCTGGGGGAGGG 1640

RESULT 5
US-09-940-235-10
; Sequence 10, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahn, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
```

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; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-09-940-235-10

Alignment Scores:
Pred. No.: 2,78e-59 Length: 1661
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-09-940-235-10 (1-1661)
Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1341 CAGCGCAGCAAAATGGTTTCAGCCCGTCCCGTGGTGTTCAGTCAAGCAAGCCCGGT 1400
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgTyrTyrLeuGly 40
Db 1401 TGTATGACAAATGGAACACATATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGT 1460
Qy 41 AsnValLeuValCysThrCysTyrGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 1461 AATGTGTTGGTTTGTACTTGTATCGAGGAAGCGAGGTTTAACTGCGAAAGTAAACCT 1520
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 1521 GAAGCTGAAGAGACTTGTCTTTGACAAGTACACTGGGACACTTACCGAGTGGTGACACT 1580
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 1581 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACTGCTCGGGCTGGGGGAGGG 1640

Qy 101 ArgIleSerCysThrIle 106
Db 1641 AGAATAAGCTGTACCATC 1658

RESULT 6
US-10-631-558-10
; Sequence 10, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahn, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
```



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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-10-631-558-10

Alignment Scores:
Pred. No.: 2,78e-59 Length: 1661
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-631-558-10 (1-1661)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1341 CAGGCGCAGCAAAATGGTTTCAGCCCAAGTCCCGGGTGGCTGTCTCAAGCAAGCCCGGT 1400

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnIntrpGluArgThrTyrLeuGly 40
Db 1401 TGTATGACATCGAAACACATATCAGATAAATCAACAGTGGGAGCGACCTACCTAGGT 1460

Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 1461 AATGTGTGGTTTGTACTGTGTATGGAGGAAGCCGAGGTTTTAACTGCGAAGTAAACCT 1520

Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 1521 GAAGCTGAAGAGACTTCTTTGACAAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 1580

Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 1581 TATGAGCGTCTCTAAAGACTCCATCATCTGGGACTGTACCTGCATCGGGCTGGGGAGGG 1640

Qy 101 ArgIleSerCysThrIle 106
Db 1641 AGAATAAGCTGTACCATC 1658

RESULT 7
US-10-236-392-1
; Sequence 1, Application US/10236392
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Caeman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K

; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 1
; LENGTH: 6988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)...(6986)
US-10-236-392-1

Alignment Scores:
Pred. No.: 1.63e-58 Length: 6988
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 49 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-236-392-1 (1-6988)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGGTTTCAGCCCAAGTCCCGGGTGGCTGTCTCAAGCAAGCCCGGT 73

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnIntrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACATCGAAACACATATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133

Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATGTGTGGTTTGTACTGTGTATGGAGGAAGCCGAGGTTTTAACTGCGAAGTAAACCT 193

Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTGTCTTTGACAAAGTACACTGGGAACACATTACCGAGTGGGTGACACT 253

Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTCTAAAGACTCCATCATCTGGGACTGTACCTGCATCGGGCTGGGGAGGG 313

Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331
```

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RESULT 8
PCT-US01-14827-4096
; Sequence 4096, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 4096
; LENGTH: 7341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(7338)
; OTHER INFORMATION: 100% homologous to Homo sapiens Fibrinogen-alpha, accession
; OTHER INFORMATION: number AAR60021, Smith-Waterman Score=13183.
PCT-US01-14827-4096

```

Alignment Scores:		
Pred. No.:	1.74e-58	
Score:	600.00	Length: 7341
Percent Similarity:	100.00%	Matches: 106
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
DB:	1	Indels: 0
		Gaps: 0

US-09-940-235-4 COPY 1 106 (1-106) x PCT-US01-14827-4096 (1-7341)

Qy	1	GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerIysProGly	20
Dd	94	CAGGCTCAGCAAAATGGTTTCAGCCCGTCCCGGTGGCTGTCACTCAAAGCAAGCCCGGT	153
Qy	21	CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnIleTrpGluArgThrTyrIeuGly	40
Dd	154	TGTTTATGACATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCCTAGGT	213
Qy	41	AsnValIleuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerIysPro	60
Dd	214	AATGTGTGGTTTGTACTTGTATGGAGAAGCCGAGGTTTTAACTGCCGAATAGTAAACCT	273
Qy	61	GluAlaGluThrCysPheAspIysTyrThrGlyAsnThrTyrArgValGlyAspThr	80
Dd	274	GAAGCTGNAGAGACTTGTTTGGACAAAGTACACTGGGAACACTTACCGAGTGGGTGCNACT	333
Qy	81	TyrGluArgProIysAspSerMetIleTrpAspCysThrCysIleGlyalaGlyArgGly	100
Dd	334	TATCAGCGTCTCAAAGACTCCCATGATCTGGGACTGTACTGTGCATCGGGGCTGGGGCAGGG	393
Qy	101	ArgIleSerCysThrIle	106
Dd	394	AGAATAAGCTGTACCATC	411

```

RESULT 9
US-09-577-408-5027
; Sequence 5027, Application US/09577408
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radjoja T.
; TITLE OF INVENTION: Novel Nucleic AC
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 792
; CURRENT APPLICATION NUMBER: US/09/577
; CURRENT FILING DATE: 2000-05-18

```

```

; NUMBER OF SEQ ID NOS: 8502
; SOFTWARE: pt_gct_genes Version 1.0
; SEQ ID NO 5027
; LENGTH: 7341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82)...(7338)
; OTHER INFORMATION: similar to g131397 in the genepept database release 115,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-577-408-5027

```

Alignment Scores:	
Pred. No.:	1,749-58
Score:	600.00
Length:	7341
Percent Similarity:	100.00%
Matches:	106
Best Local Similarity:	100.00%
Mismatches:	0
Query Match:	100.00%
Indels:	0
DB:	25
Gaps:	0

US-09-940-235-4 COPY 1 106 (1-106) X US-09-577-408-5027 (1-7341)

Qy	1	GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly	20
Db	94	CAGGCTCAGCAAAATGGTTTCAGCCCCAGTCCCGGTGGCTGTCAAGTAAAGCAAGCCCGGT	153
Qy	21	CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly	40
Db	154	TGTTATGACATATGGAAACACTATCAGATAAATCAACATGTGGAGCGGACCTTACCTAGGT	213
Qy	41	AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro	60

Db 214 AATCTGTTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTAACTGCGAAGTAAACCT 273

Qy	61	Glu	Ala	Glu	Glu	Thr	Cys	Phe	Asp	Pro	Tyr	Thr	Gly	Asn	Thr	Tyr	Arg	Val	Gly	Asp	Thr	80
Db	274	GAAGCT	GAA	GAG	ACT	TGCTTT	TGA	CAA	GTC	CAC	TGG	GAA	CAT	TAC	GAG	TGG	GGT	GAC	ACT			333

Qy	81	TyrGluArgProTyrAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly	100
Db	334	TATGAGCGTCTTAAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGGTGGCGGAGGG	393

Qy 101 ArgIleSerCysThrIle 106
|||
Db 394 AGAATAAGCTGTACCATC 411

RESULT 10
US-10-155-653-38
; Sequence 38, Application US/10155653
: GENERAL INFORMATION:

```

1 APPLICANT: SHYJIAN, ANDREW W.
2 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND
3 TITLE OF INVENTION: ASSESSMENT
4 TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF
5 FILE REFERENCE: 07334-074001
6 CURRENT APPLICATION NUMBER: US/10/155,653
7 CURRENT FILING DATE: 2002-05-23
8 PRIOR APPLICATION NUMBER: US/09/220,132
9 PRIOR FILING DATE: 1998-12-23
10 PRIOR APPLICATION NUMBER: US 60/079,303
11 PRIOR FILING DATE: 1998-03-25
12 PRIOR APPLICATION NUMBER: US 60/068,821
13 PRIOR FILING DATE: 1997-12-24
14 NUMBER OF SEQ ID NOS: 191
15 SOFTWARE: FASTSEQ for Windows Version 4.0
16 SEQ ID NO 38

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; SEQ ID NO 38
 ;
 ; LENGTH: 7679
 ;
 ; TYPE: DNA
 ;
 ; ORGANISM: Homo sapiens
 ;
 ; US-10-155-653-38

Alignment Scores:

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Pred. No.: 1.84e-58 Length: 7679
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 48 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-155-653-38 (1-7679)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGGTTGAGCCCGAGTCCCGGGTGTGAGTCAAGCAAGCCCGGT 73

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACATGGAACACATATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133

Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlySerLysPro 60
Db 134 AATGTTGGTTTGTACTTGTATGAGGAAGCCGAGGTTTAACTGCGAAAGTAAACCT 193

Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 74 TGTATGACATGGAACACATATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133

Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG 313

Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCAC 331

RESULT 11
US-10-831-704-38
Sequence 38, Application US/10831704
GENERAL INFORMATION:
APPLICANT: Shvian, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND
FILE OF INVENTION: ASSESSMENT
FILE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US/10/831,704
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US/10/155,653
PRIOR FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US/09/220,132
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 7679
TYPE: DNA
ORGANISM: Homo sapiens
US-10-831-704-38

Alignment Scores:
Pred. No.: 1.84e-58 Length: 7679
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 52 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-831-704-38 (1-7679)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGGTTGAGCCCGAGTCCCGGGTGTGAGTCAAGCAAGCCCGGT 73
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Pred. No.: 1.84e-58 Length: 7680
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US02-02176-1216 (1-7680)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGGTTGAGCCCGAGTCCCGGGTGTGAGTCAAGCAAGCCCGGT 73

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACATGGAACACATATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133

Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlySerLysPro 60
Db 134 AATGTTGGTTTGTACTTGTATGAGGAAGCCGAGGTTTAACTGCGAAAGTAAACCT 193

Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80

RESULT 12
PCT-US02-02176-1216
Sequence 1216, Application PC/TUS0202176
GENERAL INFORMATION:
APPLICANT: Orr, Michael S.
APPLICANT: Nation, Michele
APPLICANT: Diggins, James C.
APPLICANT: Zeng, Wen
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Breast Tissue
FILE REFERENCE: 44921-5070-WO
CURRENT APPLICATION NUMBER: PCT/US02/02176
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/263,757
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/286,090
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/292,517
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 1246
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1216
LENGTH: 7680
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. X02761
PCT-US02-02176-1216

Alignment Scores:
Pred. No.: 1.84e-58 Length: 7680
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US02-02176-1216 (1-7680)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGGTTGAGCCCGAGTCCCGGGTGTGAGTCAAGCAAGCCCGGT 73

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACATGGAACACATATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133

Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlySerLysPro 60
Db 134 AATGTTGGTTTGTACTTGTATGAGGAAGCCGAGGTTTAACTGCGAAAGTAAACCT 193

Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
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Db 194 GAAGCTGAAGAGACTTGTCTTACCAAGTACACTGGGAACACTTACCAGTGGGTGACACT 253
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGCGGAGGG 313
Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331
RESULT 13
PCT-US02-10824-60
; Sequence 60, Application PC/TUS0210824
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Prostate Cancer Expression Profiles
; FILE REFERENCE: 9U 206 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/10824
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/281,732
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/281,731
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-10824-60

Alignment Scores:
Pred. No.: 1.84e-58 Length: 7680
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US02-10824-60 (1-7680)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGCGCTCAGCAATGGTTTTCAGCCCGTCCCGGTGGCTGTCAAGCAAGCCCGGT 73
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACAATGGAACAACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATGTGTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTAACTGCGAAAGTAAACCT 193
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTGTCTTACCAAGTACACTGGGAACACTTACCAGTGGGTGACACT 253
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGCGGAGGG 313
Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331

RESULT 14
PCT-US02-14877A-654
; Sequence 654, Application PC/TUS0214877A
; GENERAL INFORMATION:
; APPLICANT: Genome Therapeutics Corporation and
; APPLICANT: Allen, Kristina M.
; APPLICANT: Yaworsky, Paul

; APPLICANT: Morales, Arturo J.
; APPLICANT: Graham, James R.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: Hm Variants that Modulate Bone Mass and Lipid Levels
; FILE REFERENCE: 032796-135
; CURRENT APPLICATION NUMBER: PCT/US02/14877A
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 654
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14877A-654

Alignment Scores:
Pred. No.: 1.84e-58 Length: 7680
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US02-14877A-654 (1-7680)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGCGCTCAGCAATGGTTTTCAGCCCGTCCCGGTGGCTGTCAAGCAAGCCCGGT 73
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACAATGGAACAACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATGTGTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTAACTGCGAAAGTAAACCT 193
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTGTCTTACCAAGTACACTGGGAACACTTACCAGTGGGTGACACT 253
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGCGGAGGG 313
Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331

RESULT 15
PCT-US02-15982-75
; Sequence 75, Application PC/TUS0215982
; GENERAL INFORMATION:
; APPLICANT: Allen, Kristina M.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Bhat, Bheem
; APPLICANT: Damagnez, Veronique
; APPLICANT: Robinson, John
; APPLICANT: Yaworsky, Paul
; TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
; FILE REFERENCE: 032796-132
; CURRENT APPLICATION NUMBER: PCT/US02/15982
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/291,311

Search completed: November 6, 2004, 07:38:44
Job time : 1744.21 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:38:12 ; Search time 32.8527 Seconds
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Title: US-09-940-235-4_COPY_1_106

Perfect score: 600

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 63957 seqs, 115811272 residues

Total number of hits satisfying chosen parameters: 1387914

Minimum DB seq length: 0

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Maximum Match 100%

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09940235@cgn_1.1.480 @runat_03112004_174040_11339
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
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8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	600	100.0	7680	6	US-10-948-737-4446 Sequence 4446, Ap
2	596	99.3	2127	6	US-10-956-157-4288 Sequence 4288, Ap
3	596	99.3	2402	1	PCT-US04-31524-364 Sequence 364, App
4	596	99.3	7677	6	US-10-956-157-4995 Sequence 4995, Ap
5	596	99.3	7912	1	PCT-US04-31524-366 Sequence 366, App
6	596	99.3	8272	1	PCT-US04-31524-370 Sequence 370, App
7	596	99.3	8374	1	PCT-US04-31524-374 Sequence 374, App
8	596	99.3	8449	1	PCT-US04-31524-190 Sequence 190, App
9	596	99.3	8647	1	PCT-US04-31524-368 Sequence 368, App
10	596	99.3	8815	1	PCT-US04-31524-372 Sequence 372, App

11	596	99.3	8815	6	US-10-868-577A-62 Sequence 62, Appl
12	317	52.8	407	6	US-10-964-549-799 Sequence 799, App
13	162.5	27.1	588	6	US-10-956-157-4994 Sequence 4994, App
14	162.5	27.1	588	6	US-10-956-157-10229 Sequence 10229, A
15	162.5	27.1	600	6	US-10-956-157-9521 Sequence 9521, Ap
16	162.5	27.1	1241	6	US-10-956-157-234 Sequence 234, App
17	162.5	27.1	1241	6	US-10-956-157-5469 Sequence 5469, App
18	162.5	27.1	1400	6	US-10-956-157-10230 Sequence 10230, A
19	162.5	27.1	2384	6	US-10-956-157-4286 Sequence 4286, Ap
20	147.5	24.6	607	6	US-10-948-737-12304 Sequence 12304, A
21	138.5	23.1	600	6	US-10-956-160-215929 Sequence 215929, A
22	138.5	23.1	1567	6	US-10-956-160-5822 Sequence 5822, Ap
23	135	22.5	600	6	US-10-956-157-9523 Sequence 9523, Ap
24	130.5	21.8	600	6	US-10-956-160-215928 Sequence 215928, A
25	130.5	21.8	794	6	US-10-956-160-5821 Sequence 5821, Ap
26	116.5	19.4	609	6	US-10-948-737-3916 Sequence 3916, Ap
27	93	15.5	13715	6	US-10-399-103A-365 Sequence 365, App
28	91	15.2	268	6	US-10-220-366A-7529 Sequence 7529, App
29	87	14.5	502	6	US-10-954-094-130 Sequence 130, App
30	87	14.5	775	6	US-10-954-094-116 Sequence 116, App
31	87	14.5	1032	6	US-10-954-094-98 Sequence 98, Appl
32	87	14.5	1305	6	US-10-954-094-84 Sequence 84, Appl
33	75	12.5	2853	6	US-10-961-020-3 Sequence 3, Appl1
34	75	12.5	3446	6	US-10-961-020-7 Sequence 7, Appl1
35	74	12.3	3650	6	US-10-956-157-5017 Sequence 5017, Ap
36	74	12.3	3665	6	US-10-956-157-2573 Sequence 2573, Ap
37	73	12.2	2036	6	US-10-956-157-642 Sequence 642, App
38	72.5	12.1	3201	6	US-10-650-650-17 Sequence 17, Appl
39	72.5	12.1	3657	6	US-10-650-650-2 Sequence 2, Appl1
40	72	12.0	4469	8	US-60-613-292-875 Sequence 875, App
41	71.5	11.9	2958	6	US-10-956-157-1891 Sequence 1891, Ap
42	70.5	11.8	2061	6	US-10-956-373-15 Sequence 15, Appl
43	70.5	11.8	2437	6	US-10-956-373-13 Sequence 13, Appl
44	70.5	11.7	4647	6	US-10-956-373-9 Sequence 9, Appl1
45	70	11.7	1395	6	US-10-662-425-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-948-737-4446

; Sequence 4446, Application US/10948737

; GENERAL INFORMATION:

; APPLICANT: CHAN, VIVIEN W.

; APPLICANT: ESCOBEDO, JAIME

; APPLICANT: GARCIA, PABLO DOMINGUEZ

; APPLICANT: HANSEN, RHONDA

; APPLICANT: KAUFMANN, JOERG

; APPLICANT: KENNEDY, GIULIA C.

; APPLICANT: LAMSON, GEORGE

; APPLICANT: MOLIER, EDWARD J.

; APPLICANT: RANDAZZO, FILIPPO

; APPLICANT: REINHARD, CHRISTOPH

; APPLICANT: SUDDUTH-KLINGER, JULIE

; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

; FILE REFERENCE: IN CANCEROUS CELLS III

; CURRENT FILING DATE: 2004-09-22

; PRIOR APPLICATION NUMBER: US/10/948,737

; PRIOR FILING DATE: 2004-09-22

; PRIOR APPLICATION NUMBER: 10/616,900

; PRIOR FILING DATE: 2003-07-09

; PRIOR APPLICATION NUMBER: 09/872,850

; PRIOR FILING DATE: 2001-06-01

; PRIOR APPLICATION NUMBER: 60/208,871

; PRIOR FILING DATE: 2000-06-02

; PRIOR APPLICATION NUMBER: 10/081,519

; PRIOR FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: 60/270,959

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 10/310,673

; PRIOR FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/336,613

; PRIOR FILING DATE: 2001-12-04


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Db 540 GAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 599
Qy 81 TyrGluArgProLysAspSerMetIleThrAspCysThrCysIleGlyAlaGlyArgGly 100
Db 600 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGGCTGGGCGAGGG 659
Qy 101 ArgIleSerCysThrIle 106
Db 660 AGAATAAGCTGTACCATC 677

RESULT 4
US-10-956-157-4995
; Sequence 4995, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4995
; LENGTH: 7677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4995

Alignment Scores:
Pred. No.: 9,98e-67 Length: 7677
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-956-157-4995 (1-7677)
Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGGTTTCAGCCCGAGTCCCGGTGCTGTCAAGCAAGCCCGGT 73
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnThrGluArgThrTyrLeuGly 40
Db 74 TGTATGACAATGGAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGC 133
Qy 41 AsnValIleuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATCGGTGGTTGTACTTGTATGGAGGAGCGGAGGTTTAACTCGAGAGTAAACCT 193
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 253
Qy 81 TyrGluArgProLysAspSerMetIleThrAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGGCTGGGCGAGGG 313
Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331

RESULT 5
PCT-US04-31524-366
; Sequence 366, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 8272
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-370

Alignment Scores:
Pred. No.: 1.1e-66 Length: 8272
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0

```

```

; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366
; LENGTH: 7912
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-366

Alignment Scores:
Pred. No.: 1.04e-66 Length: 7912
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-366 (1-7912)
Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAAAATGGTTTCAGCCCGAGTCCCGGTGCTGTCAAGCAAGCCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnThrGluArgThrTyrLeuGly 40
Db 420 TGTATGACAATGGAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGC 479
Qy 41 AsnValIleuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 480 AATCGGTGGTTGTACTTGTATGGAGGAGCGGAGGTTTAACTCGGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 540 GAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 599
Qy 81 TyrGluArgProLysAspSerMetIleThrAspCysThrCysIleGlyAlaGlyArgGly 100
Db 600 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGGCTGGGCGAGGG 659
Qy 101 ArgIleSerCysThrIle 106
Db 660 AGAATAAGCTGTACCATC 677

RESULT 6
PCT-US04-31524-370
; Sequence 370, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 8272
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-370

Alignment Scores:
Pred. No.: 1.1e-66 Length: 8272
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0

```


DB:	1	Gaps:	0
US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-370 (1-8272)			
QY	1	GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly	20
Db	360	CAGGCTCAGCAAAATGGTTACGCCAGTCCCGGTGGCTGTCAAGTCAAAGCAAGCCCGGT	419
QY	21	CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly	40
Db	420	TGTTATGACAATGGAAAAACACTATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGC	479
QY	41	AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro	60
Db	480	AATCGGTTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCT	539
QY	61	GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr	80
Db	540	GAAGCTGAAGAGACTTGCCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACT	599
QY	81	TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly	100
Db	600	TATGAGCGTCTCTAAAGACTCATGATCTGGGACTGTACTGCATCGGGCTGGCGGAGG	659
QY	101	ArgIleSerCysThrIle 106	
Db	660	AGAATAAGCTGTACCATC 677	
RESULT 7			
PCT-US04-31524-374			
; Sequence 374, Application PC/TUS0431524			
; GENERAL INFORMATION:			
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.			
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS			
; FILE REFERENCE: DFN-054PC			
; CURRENT APPLICATION NUMBER: PCT/US04/31524			
; CURRENT FILING DATE: 2004-10-01			
; PRIOR APPLICATION NUMBER: 60/506221			
; PRIOR FILING DATE: 2003-09-25			
; PRIOR APPLICATION NUMBER: 60/509594			
; PRIOR FILING DATE: 2003-10-08			
; NUMBER OF SEQ ID NOS: 381			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 374			
; LENGTH: 8374			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
PCT-US04-31524-374			
Alignment Scores:			
Pred. No.:	1.12e-66	Length:	8374
Score:	596.00	Matches:	105
Percent Similarity:	99.06%	Conservative:	0
Best Local Similarity:	99.06%	Mismatches:	1
Query Match:	99.33%	Indels:	0
DB:	1	Gaps:	0
US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-374 (1-8374)			
QY	1	GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly	20
Db	360	CAGGCTCAGCAAAATGGTTACGCCAGTCCCGGTGGCTGTCAAGTCAAAGCAAGCCCGGT	419
QY	21	CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly	40
Db	420	TGTTATGACAATGGAAAAACACTATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGC	479
QY	41	AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro	60
Db	480	AATCGGTTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCT	539
QY	61	GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr	80

```

Db      540 GAAGCTGAAGAGACTGCTTTGACAAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 590
Qy      81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyValaGlyArgGly 100
Db      600 TATGAGCGTCTCAAAGACTCCATGATCTGGGACTGTACTGCATCGGGCTGGGCGAGGG 659
Qy      101 ArgIleSerCysThrIle 106
Db      660 AGAATAAGCTGTACCATC 677

RESULT 8
PCT-US04-31524-190
; Sequence 190, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 8449
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-190

Alignment Scores:
Pred. No.:      1,14e-66      Length:      8449
Score:          596.00      Matches:    105
Percent Similarity: 99.06%      Conservative: 0
Best Local Similarity: 99.06%      Mismatches: 1
Query Match:      99.33%      Indels:     0
DB:              1          Gaps:     0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-190 (1-8449)

Qy      1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db      360 CAGGCTCAGCAAAATGGTTTCAGCCCGGTCCCGGTGGCTGTCACTCAAAAGCAAGCCCGGT 419
Qy      21 CysTrpAspGlnGlyLysHisTyrGlnIleAlaGlnGlnTrpGluArgThrTyrLeuGly 40
Db      420 TGTATTGACAAATGGAACAACCTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGC 479
Qy      41 AsnValLeuValCysThrCysTyrGlySerArgGlyPheAsnCysGluSerLysPro 60
Db      480 AATCGTGTGGTTGTACTTGTATTGAGGAAGCCGAGGTTTAACTGCCGAGAGTAAACCT 539
Qy      61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db      540 GAAGCTCAAGAGACTTGCTTTGACAAAGTACACTCTGGGAACACTTACCGAGTGGGTGACACT 599
Qy      81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyValaGlyArgGly 100
Db      600 TATGAGCGTCTCAAAGACTCCATGATCTGGGACTGTACTGCATCGGGCTGGGCGAGGG 659
Qy      101 ArgIleSerCysThrIle 106
Db      660 AGAATAAGCTGTACCATC 677

RESULT 9
PCT-US04-31524-368
; Sequence 368, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524

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; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 8647
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-368

Alignment Scores:
Pred. No.: 1.17e-66 Length: 8647
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservativeness: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-368 (1-8647)
Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAATGGTTTCAGCCCCAGTCCCGGCTGTCAGTCAAGCAAGCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnInTrpGluArgThrTyrLeuGly 40
Db 420 TGTATGACATGGAACACATATCAGATAAATCAACAGTGGAGCGGACCTTACCTAGGC 479
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlnSerLysPro 60
Db 480 AATGGCTTGGTTGTACTTGTATGGAGGAGCCGAGGTTTAACTGCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 540 GAAGCTGAAGAGACTTGTCTTGCACAACTACACTGGGAACACTTACCGAGTGGGTGACACT 599
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 600 TATGAGCGTCTTAAAGACTCCATGATCTGGGACTGTACCTGCGGGCTGGCGAGGG 659
Qy 101 ArgIleSerCysThrIle 106
Db 660 AGAATAAGCTGTACCATC 677

RESULT 10
PCT-US04-31524-372
; Sequence 372, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 8815
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-372

Alignment Scores:
Pred. No.: 1.2e-66 Length: 8815
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservativeness: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-372 (1-8815)
Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAATGGTTTCAGCCCCAGTCCCGGCTGTCAGTCAAGCAAGCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnInTrpGluArgThrTyrLeuGly 40
Db 420 TGTATGACATGGAACACATATCAGATAAATCAACAGTGGAGCGGACCTTACCTAGGC 479
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlnSerLysPro 60
Db 480 AATGGCTTGGTTGTACTTGTATGGAGGAGCCGAGGTTTAACTGCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
```

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Query Match: 99.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-372 (1-8815)
Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAATGGTTTCAGCCCCAGTCCCGGCTGTCAGTCAAGCAAGCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnInTrpGluArgThrTyrLeuGly 40
Db 420 TGTATGACATGGAACACATATCAGATAAATCAACAGTGGAGCGGACCTTACCTAGGC 479
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlnSerLysPro 60
Db 480 AATGGCTTGGTTGTACTTGTATGGAGGAGCCGAGGTTTAACTGCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 540 GAAGCTGAAGAGACTTGTCTTGCACAACTACACTGGGAACACTTACCGAGTGGGTGACACT 599
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 600 TATGAGCGTCTTAAAGACTCCATGATCTGGGACTGTACCTGCGGGCTGGCGAGGG 659
Qy 101 ArgIleSerCysThrIle 106
Db 660 AGAATAAGCTGTACCATC 677

RESULT 11
US-10-868-577A-62
; Sequence 62, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alicata et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 8815
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-577A-62

Alignment Scores:
Pred. No.: 1.2e-66 Length: 8815
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservativeness: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-868-577A-62 (1-8815)
Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAATGGTTTCAGCCCCAGTCCCGGCTGTCAGTCAAGCAAGCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnInTrpGluArgThrTyrLeuGly 40
Db 420 TGTATGACATGGAACACATATCAGATAAATCAACAGTGGAGCGGACCTTACCTAGGC 479
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlnSerLysPro 60
Db 480 AATGGCTTGGTTGTACTTGTATGGAGGAGCCGAGGTTTAACTGCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
```

Db 540 GAAGCTGAAGAGACTTGGCTTTTGACAAGTACACTGGGAACACTTACCAGTGGGTGACACT 599

QY 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100

Db 600 TATGAGCGCTCTTAAGACTCCATCATCTGGGACTGTACTCGGGCTGGCGGAGGG 659

QY 101 ArgIleSerCysThrIle 106

Db 660 AGAATAAGCTGTACCATC 677

RESULT 12

```

US-10-964-549-799
;
; SEQUENCE 799, Application US/10964549
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Mutated Mammalian
; FILE REFERENCE: LEX-0286-USA
; CURRENT APPLICATION NUMBER: US/10/964,549
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: US/09/750,456
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/728,445
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 799
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(407)
; OTHER INFORMATION: n = A,T,C or G
US-10-964-549-799

```

RESULT 13

RESOL 13
US-10-956-157-4994
; Sequence 4994, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS

```

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4994
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4994

```

RESULT 14

```

US-10-956-157-10229
; Sequence 10229, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounds, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAY
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 1010
; CURRENT APPLICATION NUMBER: US/10/956,
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10229
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-10229

```

Db 70 TGCCATGACATATGGTGTGAACCTACAAGATTGGAGAGAAAGTGGACCCGTACGGGAGAAAAT 129
Qy 40 GlyAsnValLeuValCysThrCysTyrGlyGlySerArgGly---PheAsnCysGluSer 58
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 130 GCCCAGATGATGAGCTGCACATGCTCTGGGAACGGAAAAGAGAAATTCAGTGTGACCCCT 189
Qy 59 LysProGluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGly 78
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 190 CAT-----GAGGCAACGTGTATGAT-----GATGGGAAGACATACCACGTAGGA 234
Qy 79 AspThrTyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGly 98
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 235 GAACAGTGGCAGAGAAGAAATATCTCGGTGCCATTGCTCTGCACATGCTTTGGAGGCCAG 294
Qy 99 ArgGly 100
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 295 CGGGGC 300

RESULT 15
US-10-956-157-9521
; Sequence 9521, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9521
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9521

Alignment Scores:
Pred. No.: 4.95e-12 Length: 600
Score: 162.50 Matches: 32
Percent Similarity: 57.32% Conservative: 15
Best Local Similarity: 39.02% Mismatches: 28
Query Match: 27.08% Indels: 7
DB: 6 Gaps: 4

US-09-940-235-4_COPY_1_106 (1-106) x US-10-956-157-9521 (1-600)

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnTrpGluArgThr---TyrLeu 39
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 190 TGCCATGACATATGGTGTGAACCTACAAGATTGGAGAGAAAGTGGACCCGTACGGGAGAAAAT 249
Qy 40 GlyAsnValLeuValCysThrCysTyrGlyGlySerArgGly---PheAsnCysGluSer 58
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 250 GCCCAGATGATGAGCTGCACATGCTCTGGGAACGGAAAAGAGAAATTCAGTGTGACCCCT 309
Qy 59 LysProGluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGly 78
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 310 CAT-----GAGGCAACGTGTATGAT-----GATGGGAAGACATACCACGTAGGA 354
Qy 79 AspThrTyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGly 98
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 355 GAACAGTGGCAGAGAAGAAATATCTCGGTGCCATTGCTCTGCACATGCTTTGGAGGCCAG 414
Qy 99 ArgGly 100
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 415 CGGGGC 420

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:21:37 ; Search time 1800.68 Seconds
(without alignments)
2477.164 Million cell updates/sec

Title: US-09-940-235-4_COPY_150_259

Perfect score: 627

Sequence: 1 PIAEKCFDHAAGTSYVVGET.....ERHTSVQTTSGSGPFTDVR 110

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 44308572 seqs, 20275418765 residues

Total number of hits satisfying chosen parameters: 88617144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Pending Patents NA Main -QFMT=fastcap -SUFFIX=p2n.rnmp -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000
-USER=US09940235_@CGN_1_10331_@runat_03112004_174040_11309 -NCFU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	627	100.0	357	21	Sequence 6693, Ap
2	627	100.0	357	21	Sequence 6818, Ap
3	627	100.0	777	21	Sequence 3, Appli
4	627	100.0	777	21	Sequence 3, Appli
5	627	100.0	777	57	Sequence 3, Appli
6	627	100.0	1446	28	Sequence 762, App
7	627	100.0	1446	28	Sequence 9663, Ap
8	627	100.0	1446	30	Sequence 10150, A
9	627	100.0	1541	21	Sequence 9, Appli
10	627	100.0	1541	40	Sequence 9, Appli
11	627	100.0	1541	57	Sequence 9, Appli
12	627	100.0	1926	25	Sequence 41, Appl
13	627	100.0	1926	25	Sequence 41, Appl
14	627	100.0	2096	21	Sequence 12, Appl
15	627	100.0	2096	40	Sequence 12, Appl
16	627	100.0	2096	57	Sequence 12, Appl
17	627	100.0	2127	2	Sequence 49, Appl
18	627	100.0	2127	116	Sequence 49, Appl
19	627	100.0	2127	116	Sequence 4288, Ap
20	627	100.0	2147	25	Sequence 2, Appli
21	627	100.0	2147	25	Sequence 2, Appli
22	627	100.0	2147	25	Sequence 2, Appli
23	627	100.0	2402	64	Sequence 1138, Ap
24	627	100.0	2402	123	Sequence 1138, Ap
25	627	100.0	2443	2	Sequence 70, Appl
26	627	100.0	2443	2	Sequence 238, App
27	627	100.0	2443	61	Sequence 238, App
28	627	100.0	2443	61	Sequence 70, Appl
29	627	100.0	2443	61	Sequence 111, App
30	627	100.0	2443	64	Sequence 1127, Ap
31	627	100.0	2443	122	Sequence 61, Appl
32	627	100.0	2443	123	Sequence 1474, Ap
33	627	100.0	2488	2	Sequence 75, Appl
34	627	100.0	2488	2	Sequence 244, App
35	627	100.0	2488	61	Sequence 244, App
36	627	100.0	2488	61	Sequence 75, Appl
37	627	100.0	2488	61	Sequence 117, App
38	627	100.0	2488	64	Sequence 1141, Ap

39 627 100.0 2488 122 US-60-568-219-67
40 627 100.0 2488 123 US-60-576-801-1487
41 627 100.0 3170 22 US-09-526-994-1167
42 627 100.0 3170 24 US-09-540-216-984
43 627 100.0 3170 26 US-09-617-603-984
44 627 100.0 4146 33 US-09-760-457-212
45 627 100.0 4146 33 US-09-760-483-269

ALIGNMENTS

RESULT 1

US-09-431-517-6693
; Sequence 6693, Application US/09431517
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-751CON1
; CURRENT APPLICATION NUMBER: US/09/431,517
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: US 09/170,294
; EARLIER FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 31760
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6693
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-431-517-6693

Alignment Scores:
Pred. No.: 1,56e-55 Length: 357
Score: 627.00% Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-940-235-4_COPY_150_259 (1-110) x US-09-431-517-6693 (1-357)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 7 CCCATAGCTGAGAGTGTTCATCATGCTGCTGGACTTCCTATGCTGCGAGAAACG 66
Qy 21 TrpGluLysProTyrGlnGlyTyrMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db 67 TGGGAGAGCCCTACCAAGGCTGGATGATGGTAGATGTTGCTGCTGGGAGAGCAGC 126
Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 127 GGAGCGATCATCTGCCTCTTAGAATAGATCAAGATCAGACACAGGACATCTAT 186
Qy 61 ArgIleGlyAspThrTrpSerIlysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 187 AGAATTGGACACCTCGAGCAGAGGAGTAAATCGAGGAACCTGCTCCAGTGCATCTGC 246
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 247 ACAGCAACGCCGAGGAGAGTGGAAAGTGTGAGAGGCACCTCTGTGAGACCAACATCG 306
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 307 AGCGATCTGCCCTTCACCGATGTTCTGT 336

RESULT 2

US-09-431-517-6818
; Sequence 6818, Application US/09431517
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-751CON1

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-09-940-235-3 (1-777)

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Qy 1 ProileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 448 CCCATAGCTGAGAAGTGTGTTGATCATGCTGCTGGACTTCCTATGTTGGTGGAGAAACG 507

Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGluGlySer 40
Db 508 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGATTGTTACTTGCCTGGGAGAAGCGCAGC 567

Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 568 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 627

Qy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 628 AGAATTGGAGACACTCGAGCAAGAGGATATCGAGGAACCTGCTCCAGTGCATCTGC 687

Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 688 ACAGCAACGCCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGCAGACACATCG 747

Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 748 AGCGGATCTGGCCCTTCACCGATGTTGCT 777
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RESULT 5

US-10-631-558-3
; Sequence 3, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 777
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(777)

US-10-631-558-3

Alignment Scores:
Pred. No.: 3,87e-55 Length: 777
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-631-558-3 (1-777)

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Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 448 CCCATAGCTGAGAAGTGTGTTGATCATGCTGCTGGACTTCCTATGTTGGTGGAGAAACG 507

Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGluGlySer 40
Db 508 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGATTGTTACTTGCCTGGGAGAAGCGCAGC 567

Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 568 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 627

Qy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 628 AGAATTGGAGACACTCGAGCAAGAGGATATCGAGGAACCTGCTCCAGTGCATCTGC 687

Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 688 ACAGCAACGCCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGCAGACACATCG 747

Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 748 AGCGGATCTGGCCCTTCACCGATGTTGCT 777
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RESULT 6

US-09-641-529-762
; Sequence 762, Application US/09641529
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1156-001
; CURRENT APPLICATION NUMBER: US/09/641,529
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,798
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 1042
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 762
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-641-529-762

Alignment Scores:
Pred. No.: 8e-55 Length: 1446
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 28 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-09-641-529-762 (1-1446)

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Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 814 CCCATAGCTGAGAAGTGTGTTGATCATGCTGCTGGACTTCCTATGTTGGTGGAGAAACG 873

Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGluGlySer 40
Db 874 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGATTGTTACTTGCCTGGGAGAAGCGCAGC 933

Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 934 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 993

Qy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 994 AGAATTGGAGACACTCGAGCAAGAGGATATCGAGGAACCTGCTCCAGTGCATCTGC 1053
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OTHER INFORMATION: Synthetically generated primer
US-09-471-349-9

Alignment Scores: 8.61e-55 Length: 1541
Pred. No.: 627.00 Matches: 110
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 21

US-09-940-235-4_COPY_150_259 (1-110) x US-09-471-349-9 (1-1541)

Qy 1 ProileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 1209 CCNATAGCTGAGAAGTGTTCATGCTGCTGGACCTCTATGTGTCGGAGAAACG 1268

Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGlySer 40
Db 1269 TGGGAGAAGCCCTACCAAGGCTGCATGATGCTAGATTGTTACTTGCCTGGGAGAAGCAGC 1328

Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 1329 GGACGCATCATCTTGCACCTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 1388

Qy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 1389 AGAATTGGAGACACCTGGAGCAAGAGGATATTCAGGAAACCTGCTCCAGTGCACTGC 1448

Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrSer 100
Db 1449 ACAGGCAACGCCGAGGAGAGTGGAGTGTGAGAGGCACACCTCTGTGCAGACCATCG 1508

Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 1509 AGCGGATCTGCCCTTCACCGATGTTGCT 1538

RESULT 10
US-09-940-235-9
; Sequence 9, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-09-940-235-9

Alignment Scores: 8.61e-55 Length: 1541
Pred. No.: 627.00 Matches: 110
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 21

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40

US-09-940-235-4_COPY_150_259 (1-110) x US-09-940-235-9 (1-1541)

Qy 1 ProileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 1209 CCNATAGCTGAGAAGTGTTCATGCTGCTGGACCTCTATGTGTCGGAGAAACG 1268

Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGlySer 40
Db 1269 TGGGAGAAGCCCTACCAAGGCTGCATGATGCTAGATTGTTACTTGCCTGGGAGAAGCAGC 1328

Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 1329 GGACGCATCATCTTGCACCTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 1388

Qy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 1389 AGAATTGGAGACACCTGGAGCAAGAGGATATTCAGGAAACCTGCTCCAGTGCACTGC 1448

Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrSer 100
Db 1449 ACAGGCAACGCCGAGGAGAGTGGAGTGTGAGAGGCACACCTCTGTGCAGACCATCG 1508

Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 1509 AGCGGATCTGCCCTTCACCGATGTTGCT 1538

RESULT 11
US-10-631-558-9
; Sequence 9, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-10-631-558-9

Alignment Scores: 8.61e-55 Length: 1541
Pred. No.: 627.00 Matches: 110
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 57

US-09-940-235-4_COPY_150_259 (1-110) x US-10-631-558-9 (1-1541)

Qy	1	ProilAaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr	20
Db	1209	CCCATAGCTCAGAAAGTGTTTTGATCATGCTGCTGGGACATTCCTATGTGGTTCGAGAAACG	1368
Qy	21	TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysIeuGlyGlySer	40
Db	1269	TGGGAGAAGCCCTACCAAGCTCGATGATGGTAGATTGTACTTTCCTGGGAGAAGCGACG	1328
Qy	41	GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr	60
Db	1329	GGACGGCATCACTTGCACCTTCAGAAATAGATGCAACGATCAGGACCAAGGACATCCTAT	1388
Qy	61	ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysIleCys	80
Db	1389	AGAAITGGAGACACTTGGAGCAGAGAGATATCGAGGAACCTGCTCCNGTCGATCTGC	1448
Qy	81	ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer	100
Db	1449	ACAGGCAACGGCCGAGGAGGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG	1508
Qy	101	SerGlySerGlyProPhetheThrAspValArg	110
Db	1509	AGCGGATCTGGCCCTTCACCGATGTCGT	1538

```

RESULT 12
US-09-581-651B-41
; Sequence 41, Application US/09581651B
; GENERAL INFORMATION:
; APPLICANT: University of Dundee, University of Dundee
; TITLE OF INVENTION: Polypeptides, Polynucleotides and Uses Thereof
; FILE REFERENCE: 350013-72
; CURRENT APPLICATION NUMBER: US/09/581,651B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/GB98/03766
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-581-651B-41

```

Alignment Scores:			
Pred. No.:	1.12e-54	Length:	1926
Score:	627.00	Matches:	110
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-09-940-235-4 COPY 150 259 (1-110) x US-09-581-651B-41 (1-1926)

[illegible]

```

Qy      101 SetGlySerGlyProPheThrAspValArg 110
Db      |||||
841 AGCGATCTGGCCCTTCACCGATGTTCGT 870

RESULT 13
US-09-581-651C-41
; Sequence 41, Application US/09581651C
; GENERAL INFORMATION:
; APPLICANT: Schor, Seth Lawrence
; TITLE OF INVENTION: Polypeptides, Polynucleotides and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: EP01.003APC
; CURRENT APPLICATION NUMBER: US/09/581.651C
; CURRENT FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: PCT/GB98/03766
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: GB 9726539.1
; - PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-581-651C-41

Alignment Scores:
Pred. No.:          1-12e-54           Length:       1926
Score:             627.00              Matches:       110
Percent Similarity: 100.00%            Conservative:   0
Best Local Similarity: 100.00%         Mismatches:    0
Query Match:       100.00%             Indels:        0
DB:                25                  Gaps:          0

US-09-940-235-4_COPY_150_259 (1-110) x US-09-581-651C-41 (1-1926)

Qy      1 ProIleAlaGluLysCysPheAspHisAlaAalaGlyThrSerTyrValValGlyGluThr 20
Db      |||||
541 CCATAGCTGAGAAGTGTTTTTGATCATGCTGTGGAGCTTCTCTATGTGTCGGAGAAACG 600

Qy      21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db      |||||
601 TGGAGAGAGCCCTACCAGAGCTGGATGATGATGATTGTACTTGCCTGGAGAGAGGCACG 660

Qy      41 GlyArgIleThrCysThrSerArGAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db      |||||
661 GGAGCATCACTTGCACCTTTCTAGAAATAGATGCCAACGATCAGGACACAAGGACATCTCAT 720

Qy      61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db      |||||
721 AGAATTGGAGACACCTTGGAGCAAAGAGATAATCGAGAAAACCTGCTCCAGTGCATCTGC 780

Qy      81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db      |||||
781 ACAGGCACCGCCGAGGAGAGTGGAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 840

Qy      101 SerGlySerGlyProPheThrAspValArg 110
Db      |||||
841 AGCGATCTGGCCCTTCACCGATGTTCGT 870

```

RESULT 14
US-09-471-349-12
; Sequence 12, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: ROY, Chaiti
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir

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OM protein - protein search, using sw model

Run on: November 3, 2004, 23:49:35 ; Search time 4.14384 Seconds
(without alignments)
419.494 Million cell updates/sec

Title: US-09-940-235-4_COPY_150_259

Perfect score: 627

Sequence: 1 PIAKCFDHAAGTSYVVGCT.....ERHTSVQTTSSGSGPFTDVR 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 66696 seqs, 15802848 residues

Total number of hits satisfying chosen parameters: 66696

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	627	100.0	657	1	PCT-US04-31524-365
2	627	100.0	2176	1	PCT-US04-31524-367
3	627	100.0	2296	1	PCT-US04-31524-371
4	627	100.0	2330	1	PCT-US04-31524-375
5	627	100.0	2355	1	PCT-US04-31524-191
6	627	100.0	2386	6	US-10-868-577A-59
7	627	100.0	2421	1	PCT-US04-31524-369
8	627	100.0	2476	1	PCT-US04-31524-373
9	213	34.0	211	6	US-10-868-577A-58
10	71.5	11.4	2157	6	US-10-960-275-2
11	70	11.2	1036	6	US-10-955-952-142
12	70	11.2	1036	6	US-10-157-779-142
13	70	11.2	1036	6	US-10-964-241-142
14	69.5	11.1	950	6	US-10-961-020-4
15	69	11.0	457	6	US-10-960-275-5
16	67	10.7	454	6	US-10-732-923-13429
17	67	10.7	802	6	US-10-732-923-13428
18	65	10.4	494	6	US-10-866-527-98
19	64	10.2	796	6	US-10-882-029-24
20	64	10.2	799	6	US-10-482-029-26
21	63.5	10.1	2871	6	US-10-967-702-390
22	62	9.9	201	6	US-10-732-923-14745
23	62	9.9	240	6	US-10-732-923-14746
24	61.5	9.8	54	4	US-08-828-323A-24
25	61.5	9.8	1067	6	US-10-650-650-18

ALIGNMENTS

RESULT 1

PCT-US04-31524-365

; Sequence 365, Application PC/TUS0431524

; GENERAL INFORMATION:

; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.

; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS

; FILE REFERENCE: DEN-054PC

; CURRENT APPLICATION NUMBER: PCT/US04/31524

; CURRENT FILING DATE: 2004-10-01

; PRIOR APPLICATION NUMBER: 60/506221

; PRIOR FILING DATE: 2003-09-25

; PRIOR APPLICATION NUMBER: 60/509594

; PRIOR FILING DATE: 2003-10-08

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 365

; LENGTH: 657

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US04-31524-365

Query Match 100.0%; Score 627; DB 1; Length 657;

Best Local Similarity 100.0%; Pred. No. 7.2e-56;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PIAKCFDHAAGTSYVVGCTWEKPYQGMWVDCTCLGSGSGRITCTSRNRCNDQDTRTSY 60

Db 181 PIAKCFDHAAGTSYVVGCTWEKPYQGMWVDCTCLGSGSGRITCTSRNRCNDQDTRTSY 240

Qy 61 RIGTWSKKDNRGNLLQICITGNGRGWKCERHTSVQTTSSGSGPFTDVR 110

Db 241 RIGTWSKKDNRGNLLQICITGNGRGWKCERHTSVQTTSSGSGPFTDVR 290

RESULT 2

PCT-US04-31524-367

; Sequence 367, Application PC/TUS0431524

; GENERAL INFORMATION:

; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.

; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS

; FILE REFERENCE: DEN-054PC

; CURRENT APPLICATION NUMBER: PCT/US04/31524

; CURRENT FILING DATE: 2004-10-01

; PRIOR APPLICATION NUMBER: 60/506221

; PRIOR FILING DATE: 2003-09-25

; PRIOR APPLICATION NUMBER: 60/509594

; PRIOR FILING DATE: 2003-10-08

; NUMBER OF SEQ ID NOS: 381

Sequence 20, Appl
Sequence 54, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 4306, Ap
Sequence 137, App
Sequence 15, Appl
Sequence 45, Appl
Sequence 639, App
Sequence 6, Appl
Sequence 4, Appl
Sequence 19356, A
Sequence 2, Appl
Sequence 3075, Ap
Sequence 3170, Ap
Sequence 3245, Ap
Sequence 3244, Ap
Sequence 22435, A
Sequence 9905, Ap
Sequence 818, App

Query Match 100.0%; Score 627; DB 6; Length 2386;
Best Local Similarity 100.0%; Pred. No. 2.9e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PIAKCFDHAAGTSYVVGTEWKEPYQGMWVDCTCLGEGSGRITCTSRNRCNDQDTRTSY 60
DB 181 PIAKCFDHAAGTSYVVGTEWKEPYQGMWVDCTCLGEGSGRITCTSRNRCNDQDTRTSY 240

QY 61 RIGTWSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVR 110
DB 241 RIGTWSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVR 290

RESULT 7
PCT-US04-31524-369
; Sequence 369, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369
; LENGTH: 2421
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-369

Query Match 100.0%; Score 627; DB 1; Length 2421;
Best Local Similarity 100.0%; Pred. No. 3e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PIAKCFDHAAGTSYVVGTEWKEPYQGMWVDCTCLGEGSGRITCTSRNRCNDQDTRTSY 60
DB 181 PIAKCFDHAAGTSYVVGTEWKEPYQGMWVDCTCLGEGSGRITCTSRNRCNDQDTRTSY 240

QY 61 RIGTWSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVR 110
DB 241 RIGTWSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVR 290

RESULT 8
PCT-US04-31524-373
; Sequence 373, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 2476
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-373

Query Match 100.0%; Score 627; DB 1; Length 2476;
Best Local Similarity 100.0%; Pred. No. 3e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PIAKCFDHAAGTSYVVGTEWKEPYQGMWVDCTCLGEGSGRITCTSRNRCNDQDTRTSY 60
DB 180 PIAKCFDHAAGTSYVVGTEWKEPYQGMWVDCTCLGEGSGRITCTSRNRCNDQDTRTSY 239
QY 61 RIGTWSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVR 110
DB 240 RIGTWSKKNRGNLLQICITGNRGWKCERHTSVQTTSSGSGPFTDVR 289

RESULT 9
US-10-868-577A-58
; Sequence 58, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-58

Query Match 34.0%; Score 213; DB 6; Length 211;
Best Local Similarity 37.6%; Pred. No. 9.5e-15;
Matches 35; Conservative 17; Mismatches 39; Indels 2; Gaps 1;

QY 1 PIAKCFDHAAGTSYVVGTEWKEPYQGMWVDCTCLGEGSGRITCTSRNRCNDQDTRTSY 60
DB 26 PTDDSCFDPYTVSHYAVGDEWERMESGFKLLCQLGFGSGHFRCDSSRWCHDNG--VNY 83

QY 61 RIGTWSKKNRGNLLQICITGNRGWKCERH 93
DB 84 KIGEKWDKQNGQGMMSCTCLNGKGKFCDPH 116

RESULT 10
US-10-960-275-2
; Sequence 2, Application US/10960275
; GENERAL INFORMATION:
; APPLICANT: Hastings, et al.
; TITLE OF INVENTION: Novel Hyaluronan-Binding Proteins and Encoding Genes
; FILE REFERENCE: PF487
; CURRENT APPLICATION NUMBER: US/10/960,275
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/466,778
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/113,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: MISC FEATURE
; NAME/KEY: LOCATION: (2058)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE: MISC FEATURE
; NAME/KEY: LOCATION: (2109)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE: MISC FEATURE
; NAME/KEY: LOCATION: (2120)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (2122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (2123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-960-275-2

Query Match 11.4%; Score 71.5; DB 6; Length 2157;
Best Local Similarity 30.6%; Pred. No. 21;
Matches 30; Conservative 9; Mismatches 28; Indels 31; Gaps 7;
Qy 2 IAECDFHAGTSVVGTEWKPQGMWVDCICLG--EGSGRITCTSRNCRNDQRTS 59
Db 1678 VADLCQDHGCGCSEHANC-----QVGTMTCTCLPDYEGDG-WSCRARNPCTD----- 1725
Qy 60 YRIGDTWSKKDNKGNLLQ---CICGTG-NRGKWKCRH 93
Db 1726 -----GHRGCGSEHANCSTGLNTR---RCECH 1750

RESULT 11
US-10-955-952-142
; Sequence 142, Application US/10955952
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C12
; CURRENT APPLICATION NUMBER: US/10/955,952
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: US/10/121,058
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 142

; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-955-952-142
Query Match 11.2%; Score 70; DB 6; Length 1036;
Best Local Similarity 26.5%; Pred. No. 13;
Matches 31; Conservative 8; Mismatches 26; Indels 52; Gaps 8;
Qy 9 HAAGTSYVV-CETWEKPYQGMWVD---CTCLGSGSGRITCTSR----- 48
Db 680 HAPGEYFVEGETWN-----IDSCYQCTC---HSRVLCTEVECPPLLCQNSRTOD 728
Qy 49 ---NRCDNDQRTSYRIGDTWSKKDNKGNLLQCICTGNRGE-----WKGERHTS 95
Db 729 SCCQCTDQPPPSL-----SRNNSVPNYCK-NDEGDIPLAAESWKPDVCTS 774
RESULT 12
US-10-157-779-142
; Sequence 142, Application US/10157779
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C426
; CURRENT APPLICATION NUMBER: US/10/157,779
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 142
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-157-779-142
Query Match 11.2%; Score 70; DB 6; Length 1036;

Best Local Similarity 26.5%; Pred. No. 13;
Matches 31; Conservative 8; Mismatches 26; Indels 52; Gaps 8;

Qy 9 HAAGTSVW-GETWEKPYQGMVMD---CTCLGEGSGRITCTSR-----WKCRHSTS 95
Db 680 HAPGGYFVEGETWN-----IDSTQCTC---HSGRVLCTEVCVCPPLLCQNPSRTQD 728

Qy 49 ---NRCDQDTRTSYRIGDTWSKKDNRGNLLQICITGNRGE-----WKCRHSTS 95
Db 729 SCCPQCTDQPPRPSL-----SRNNSVPNYCK-NDEGDIFLAESWKPDVCTS 774

RESULT 13
US-10-964-241-142
; Sequence 142, Application US/10964241
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C33
; CURRENT APPLICATION NUMBER: US/10/964,241
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PRIORT APPLICATION NUMBER: US/10/123,236
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 142
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-964-241-142

Query Match 11.2%; Score 70; DB 6; Length 1036;
Best Local Similarity 26.5%; Pred. No. 13;
Matches 31; Conservative 8; Mismatches 26; Indels 52; Gaps 8;

Qy 9 HAAGTSVW-GETWEKPYQGMVMD---CTCLGEGSGRITCTSR-----WKCRHSTS 95
Db 680 HAPGGYFVEGETWN-----IDSTQCTC---HSGRVLCTEVCVCPPLLCQNPSRTQD 728

Best Local Similarity 26.5%; Pred. No. 13;
Matches 31; Conservative 8; Mismatches 26; Indels 52; Gaps 8;

Qy 49 ---NRCDQDTRTSYRIGDTWSKKDNRGNLLQICITGNRGE-----WKCRHSTS 95
Db 729 SCCPQCTDQPPRPSL-----SRNNSVPNYCK-NDEGDIFLAESWKPDVCTS 774

RESULT 14
US-10-961-020-4
; Sequence 4, Application US/10961020
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0241-USA
; CURRENT APPLICATION NUMBER: US/10/961,020
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/965,631
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/236,689
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 950
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-961-020-4

Query Match 11.1%; Score 69.5; DB 6; Length 950;
Best Local Similarity 19.7%; Pred. No. 14;
Matches 25; Conservative 18; Mismatches 45; Indels 39; Gaps 5;

Qy 12 GTSYVVGETWEK-----PYQGMVMDCT---CLGEGSGRITCTSRN-----49
Db 439 GASYTLQQCLAFGFGVSKPCPY-----MQYCTKLMCTGKAKGMVCOIRHFPWADGTSFG 494

Qy 50 -----RCNDQDTRTSYRIGDTWSKKDNRGNLLQICITGNRGEWKCRHSTSQTSS 101
Db 495 EGKCLKGCACVERHNLKRVDSWAKWDPYGP-----CSRCTGGGVQLARRQCTNPTPA 549

Qy 102 GSGPPTD 108
Db 550 NGKYCE 556

RESULT 15
US-10-960-275-5
; Sequence 5, Application US/10960275
; GENERAL INFORMATION:
; APPLICANT: Hastings, et al.
; TITLE OF INVENTION: Novel Hyaluronan-Binding Proteins and Encoding Genes
; FILE REFERENCE: PF487
; CURRENT APPLICATION NUMBER: US/10/960,275
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/466,778
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/113,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (358)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (409)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:

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; NAME/KEY: MISC FEATURE
; LOCATION: (420)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (422)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (423)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-960-275-5

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Query Match      11.0%; Score 69; DB 6; Length 457;
Best Local Similarity 34.3%; Pred. No. 6.8;
Matches 24; Conservative 6; Mismatches 14; Indels 26; Gaps 6;

Qy 30 MVDCTCLG--EGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKNRGNLLQ---CICIG-N 83
Db 1 MVTCTCLPDYEGDG-WSCRARNPCTD-----GHRGGCSEHANCILSTGLN 43

Qy 84 GRGEWKCEH 93
Db 44 TR---RCECH 50

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Search completed: November 4, 2004, 00:11:50
Job time : 5.14384 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2004, 23:49:35 ; Search time 3.99315 Seconds
(without alignments)
419.494 Million cell updates/sec

Title: US-09-940-235-4_COPY_1_106

Perfect score: 600

Sequence: 1 QAQMVPQSPVAVSQSKPG.....SMIWDCTCIGAGRISCTI 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 66696 seqs, 15802848 residues

Total number of hits satisfying chosen parameters: 66696

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	596	99.3	657	1	PCT-US04-31524-365
2	596	99.3	2176	1	PCT-US04-31524-367
3	596	99.3	2296	1	PCT-US04-31524-371
4	596	99.3	2330	1	PCT-US04-31524-375
5	596	99.3	2355	1	PCT-US04-31524-191
6	596	99.3	2386	6	US-10-868-577A-59
7	596	99.3	2421	1	PCT-US04-31524-369
8	596	99.3	2476	1	PCT-US04-31524-373
9	162.5	27.1	211	6	US-10-868-577A-58
10	93	15.5	43	6	US-10-220-366A-21430
11	93	15.5	4315	6	US-10-399-103A-811
12	75.5	12.6	1238	6	US-10-765-727-21
13	75.5	12.6	1238	6	US-10-846-989-55
14	75	12.5	950	6	US-10-961-020-4
15	72.5	12.1	1067	6	US-10-650-650-18
16	72.5	12.1	1218	6	US-10-765-727-20
17	72.5	12.1	1218	6	US-10-846-989-54
18	72.5	12.1	1218	6	US-10-650-650-1
19	71.5	11.9	2556	6	US-10-765-727-22
20	71.5	11.9	2556	6	US-10-846-989-56
21	70.5	11.8	376	6	US-10-732-923-12305
22	69.5	11.6	2471	6	US-10-765-727-23
23	69.5	11.6	2471	6	US-10-846-989-57
24	68.5	11.4	394	6	US-10-732-923-12479
25	68	11.3	167	6	US-10-954-094-131

26	68	11.3	258	6	US-10-954-094-117	Sequence 117, App
27	68	11.3	343	6	US-10-954-094-99	Sequence 99, Appl
28	68	11.3	434	6	US-10-954-094-85	Sequence 85, Appl
29	67.5	11.2	314	6	US-10-639-194-6	Sequence 6, Appli
30	67.5	11.2	394	6	US-10-732-923-12781	Sequence 12781, A
31	67.5	11.2	685	6	US-10-765-727-19	Sequence 19, Appl
32	67.5	11.2	685	6	US-10-846-989-53	Sequence 53, Appl
33	67.5	11.2	685	6	US-10-955-952-88	Sequence 88, Appl
34	67.5	11.2	685	6	US-10-157-779-88	Sequence 88, Appl
35	67.5	11.2	685	6	US-10-964-241-88	Sequence 88, Appl
36	67	11.2	2871	6	US-10-967-702-390	Sequence 390, App
37	66.5	11.1	394	6	US-10-732-923-12466	Sequence 12466, A
38	65.5	10.9	376	6	US-10-732-923-12280	Sequence 12280, A
39	65.5	10.9	392	6	US-10-732-923-12559	Sequence 12559, A
40	65.5	10.9	394	6	US-10-732-923-12806	Sequence 12806, A
41	65.5	10.9	394	6	US-10-732-923-12854	Sequence 12854, A
42	65.5	10.9	394	6	US-10-732-923-12855	Sequence 12855, A
43	64.5	10.8	394	6	US-10-732-923-12807	Sequence 12807, A
44	64.5	10.8	995	6	US-10-732-923-13678	Sequence 13678, A
45	64.5	10.8	1004	6	US-10-732-923-13677	Sequence 13677, A

ALIGNMENTS

RESULT 1
PCT-US04-31524-365
; Sequence 365, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-365

Query Match	99.3%	Score 596;	DB 1;	Length 657;
Best Local Similarity	99.1%	Pred. No. 2.8e-54;		
Matches 105;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			
Oy	1	QAQMVPQSPVAVSQSKPGCYDNGKHQIQINQWERTYILGNVLVCTCYGSGRGNCESKP	60	
Db	32	QAQMVPQSPVAVSQSKPGCYDNGKHQIQINQWERTYILGNVLVCTCYGSGRGNCESKP	91	
Oy	61	EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRISCTI	106	
Db	92	EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRISCTI	137	

RESULT 2
PCT-US04-31524-367
; Sequence 367, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381

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! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 367
! LENGTH: 2176
! TYPE: PRT
! ORGANISM: Homo sapiens
PCT-US04-31524-367

Query Match          99.3%; Score 596; DB 1; Length 2176;
Best Local Similarity 99.1%; Pred. No. 1.1e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGNVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGNVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 3
PCT-US04-31524-371
! Sequence 371, Application PC/TUS0431524
! GENERAL INFORMATION:
! APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
! TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
! FILE REFERENCE: DFN-054PC
! CURRENT APPLICATION NUMBER: PCT/US04/31524
! CURRENT FILING DATE: 2004-10-01
! PRIOR APPLICATION NUMBER: 60/506221
! PRIOR FILING DATE: 2003-09-25
! PRIOR APPLICATION NUMBER: 60/509594
! PRIOR FILING DATE: 2003-10-08
! NUMBER OF SEQ ID NOS: 381
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 371
! LENGTH: 2296
! TYPE: PRT
! ORGANISM: Homo sapiens
PCT-US04-31524-371

Query Match          99.3%; Score 596; DB 1; Length 2296;
Best Local Similarity 99.1%; Pred. No. 1.1e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGNVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGNVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 4
PCT-US04-31524-375
! Sequence 375, Application PC/TUS0431524
! GENERAL INFORMATION:
! APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
! TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
! FILE REFERENCE: DFN-054PC
! CURRENT APPLICATION NUMBER: PCT/US04/31524
! CURRENT FILING DATE: 2004-10-01
! PRIOR APPLICATION NUMBER: 60/506221
! PRIOR FILING DATE: 2003-09-25
! PRIOR APPLICATION NUMBER: 60/509594
! PRIOR FILING DATE: 2003-10-08
! NUMBER OF SEQ ID NOS: 381
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 375
! LENGTH: 2330
! TYPE: PRT
! ORGANISM: Homo sapiens
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PCT-US04-31524-375

Query Match          99.3%; Score 596; DB 1; Length 2330;
Best Local Similarity 99.1%; Pred. No. 1.1e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGNVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGNVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 5
PCT-US04-31524-191
! Sequence 191, Application PC/TUS0431524
! GENERAL INFORMATION:
! APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
! TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
! FILE REFERENCE: DFN-054PC
! CURRENT APPLICATION NUMBER: PCT/US04/31524
! CURRENT FILING DATE: 2004-10-01
! PRIOR APPLICATION NUMBER: 60/506221
! PRIOR FILING DATE: 2003-09-25
! PRIOR APPLICATION NUMBER: 60/509594
! PRIOR FILING DATE: 2003-10-08
! NUMBER OF SEQ ID NOS: 381
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 191
! LENGTH: 2355
! TYPE: PRT
! ORGANISM: Homo sapiens
PCT-US04-31524-191

Query Match          99.3%; Score 596; DB 1; Length 2355;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGNVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGNVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 6
US-10-868-577A-59
! Sequence 59, Application US/10868577A
! GENERAL INFORMATION:
! APPLICANT: Alitalo et al.
! TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
! FILE REFERENCE: 28967/39359A
! CURRENT APPLICATION NUMBER: US/10/868,577A
! CURRENT FILING DATE: 2004-06-14
! PRIOR APPLICATION NUMBER: US 60/478,390
! PRIOR FILING DATE: 2003-06-12
! PRIOR APPLICATION NUMBER: US 10/669,176
! PRIOR FILING DATE: 2003-09-23
! NUMBER OF SEQ ID NOS: 69
! SOFTWARE: Patent in version 3.2
! SEQ ID NO 59
! LENGTH: 2386
! TYPE: PRT
! ORGANISM: Homo sapiens
! FEATURE:
! NAME/KEY: misc feature
! LOCATION: (52)..(272)
! OTHER INFORMATION: heparin binding domain
US-10-868-577A-59
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Query Match 99.3%; Score 596; DB 6; Length 2386;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPSVAVSQSPGKGYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCESKP 60
Db 32 QAOQWQPSVAVSQSPGKGYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCESKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 137

RESULT 7

PCT-US04-31524-369
; Sequence 369, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DEN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369
; LENGTH: 2421
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-369

Query Match 99.3%; Score 596; DB 1; Length 2421;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPSVAVSQSPGKGYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCESKP 60
Db 32 QAOQWQPSVAVSQSPGKGYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCESKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 137

RESULT 8

PCT-US04-31524-373
; Sequence 373, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DEN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 2476
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-373

Query Match 99.3%; Score 596; DB 1; Length 2476;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPSVAVSQSPGKGYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCESKP 60
Db 31 QAOQWQPSVAVSQSPGKGYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCESKP 90
Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 106
Db 91 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 136

RESULT 9

US-10-868-577A-58
; Sequence 58, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-58

Query Match 27.1%; Score 162.5; DB 6; Length 211;
Best Local Similarity 39.0%; Pred. No. 5e-10;
Matches 32; Conservative 15; Mismatches 28; Indels 7; Gaps 4;

Qy 21 CYDNGKHQYINQWERTYLGVLVCTCYGSGRG-FNCESKPEABETCFDKYTGNTYRVG 78
Db 76 CHDNGVNYKIGEKWDROGNGQWMSCTCLGNGKGFEKCDPH---EATCYD--DGKTYHVG 130
Qy 79 DTYERPKDSMIWDCICIGAGRG 100
Db 131 EQWQKEYLGAICCTCFGGQRG 152

RESULT 10

US-10-220-366A-21430
; Sequence 21430, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 21430
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(43)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-21430

Query Match 15.5%; Score 93; DB 6; Length 43;
Best Local Similarity 48.8%; Pred. No. 0.0013;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;
Qy 59 KPEABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRG 99

DB 3 KPEKTCFDNITGNTYPCLSYEHDSDXYYVNRTXLCAER 43

RESULT 11

```

US-10-399-103A-811
; Sequence 811, Application US/10399103A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-115/ 785
; CURRENT APPLICATION NUMBER: US/10/399,103A
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: PCT/US01/27760
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/687,527
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: Custom
; SEQ ID NO 811
; LENGTH: 4315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-103A-811

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```

Query Match      15.5%; Score 93; DB 6; Length 4315;
Best Local Similarity 31.8%; Pred. No. 0.22;
Matches 30; Conservative 12; Mismatches 39; Indels 14; Gaps 5;

QY 8 PQSPFVAVSQS-----KPCYDNGHYIQNQWERTYLGVLVCTCYGSGRGFNCSEKP 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3540 PTPSPVPVSSAPLSSPSPGACDINAIPURQWETWT-----LNCITVARCVGNRVLLDPKP 3596
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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61 EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCI 95

3597 VANVTCVNKHL--PIKVSDP-SOPCD-FHYECECI 3627

RESULT 12

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US-10-765-727-21
; Sequence 21, Application US/10765727
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: YOUNG, LESLEY LYNN
; TITLE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
; FILE REFERENCE: 674525-2010
; CURRENT APPLICATION NUMBER: US/10/765,727
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: PCT/GB02/03426
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: GB 0118153.6
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: GB 0207930.9
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB 0212282.8
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: GB 0212283.6
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-765-727-21

```

Query Match 12.6%; Score 75.5; DB 6; Length 1238;
Best Local Similarity 27.8%; Pred. No. 3.5;
Matches 25; Conservative 8; Mismatches 30; Indels 27; Gaps 6;
QY 21 CYDNGKHQIQINQWERTYLGNIIVCTCYGSGRGFNCSKPEASETCFDKYT-----GNTYR 76

Db	683	CHSRGRCYD-----LVNDFYCADDGWKGKTC	HSR---EFQC-DAYTCSNGGTCYD	729
Qy	77	VGTYERPDKSMIWDCTCIGAGRGRI	SCTI	106
Db	730	SGGTFR-----CACPPQWKG	S-TCAV	749

RESULT 13

```

US-10-846-989-55
; Sequence 55, Application US/10846989
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: BREND, EMMANUEL CYRILLE PASC
; APPLICANT: CHAMPTON, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: RAGNO, SILVIA
; APPLICANT: TUGAL, TAMARA
; APPLICANT: YOUNG, LESLEY LYNN
; FILE OF INVENTION: MEDICAL TREATMENT
; TITLE REFERENCE: 654525-2012
; CURRENT APPLICATION NUMBER: US/10/846,989
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/GS02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0127271.5
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 55
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-846-989-55

```

	Query Match	12.6%	Score 75.5	DB 6	Length 1238
	Best Local Similarity	27.8%	Fred. No. 3.5	Indels 27	Gaps 6
	Matches 25	Conservative	8	Mismatches 30	
Qy	21	CYDNGKHYYIQOWERTYGLNVLVCTCYGSGRGNCSPKEAETCFDKYT	----	GNYYR	76
Db	683	CHSRGRCYD-----LVNDFYFACDDGWMGKTCHSR---	EFQC-DAYTC	SGNGTCTYD	729
Qy	77	VGDTYRPRKDSMIWDCTCIGAGRGRI	SCTI	106	
Db	730	SGPTFR-----CACPPGWKGS-TC	AV	749	

RESULT 14

```

US-10-961-020-4
; Sequence 4, Application US/10961020
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0241-USA
; CURRENT APPLICATION NUMBER: US/10/961,020
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/965,631
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/236,689
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 950
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-961-020-4

```

Query Watch	12.5%;	Score 75;	DB 6;	Length 950;
Best Local Similarity	24.6%;	Pred. No. 2.9;		
Matches 32;	Conservative 24;	Mismatches 32;	Indels 42;	Gaps 11;
QY	7	QPSPVAVSQSKPGCYDNKGHYIQNOOWERTY--LGN-----VLVCT---CYGSGRG-FNC	56	
Db	426	QPSKPISLPDLPGA-----SYTLSQOCELAFGVGSKPCPYQYCTKLWCTGKAKGMQVC	480	
QY	57	ESK--PEASEET-----CFPKYTGNTYRVGDTYERPKDSMIWD---C--TCIG	96	
Db	481	QTFHPFWADGTSQGEKGLCLKGACVERHNLNKHVRDGSWAK-----WDPYGPCSRTCGG	534	
QY	97	AGR-GRISCT	105	
Db	535	GVOLARROCT	544	

```

RESULT 15
US-10-650-650-18
; Sequence 18, Application US/10650650
; GENERAL INFORMATION:
; APPLICANT: MACIAG, Thomas
; APPLICANT: ZIMRIN, Ann
; APPLICANT: SMALL, Deena
; APPLICANT: PRUDOVSKY, Igor
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG
; FILE REFERENCE: 053689-5002-01
; CURRENT APPLICATION NUMBER: US/10/650,650
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US/09/579,536
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/199,865
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US97/09407
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/018,841
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1067
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-650-650-18

```

Query Match	12.1%;	Score 72.5;	DB 6;	Length 1067;
Best Local Similarity	24.3%;	Pred. No. 6;		
Matches	27;	Conservative 7;	Mismatches 40;	Indels 37; Gaps 6;

QY	21	CVDNGKHYO--INQWERYT-----	LGNLVCTCYGSGRGENCE	57
Db	644	CIDGVNSYKICSDGWEGAYCETIN	INDCSQNPCHNGGTCTRDLVDF	703
QY	58	SKPEA--ETCFDKYTGNTYRVGDT	VERPKDSMIWDCTCIGAGRGISCTI	106
Db	704	SRDSQDCEATC--NNGGTCTYDEGDA	RFK-----CMCPGGWEG--TTCTNI	742

Search completed: November 4, 2004, 00:11:49
Job time : 4.99315 secs